

09 828302

TI Protein and cDNA sequence of *Physcomitrella patens* signal transduction stress-related proteins and uses in plants for increased tolerance to environmental stresses

IN ***Da Costa e Silva, Oswaldo*** ; ***Bohnert, Hans J.*** ; ***Van***
*** Thielen, Nocha*** ; ***Chen, Ruoying*** ; ***Ishitani, Manabu***

PA BASF Plant Science G.m.b.H., Germany

SO PCT Int. Appl., 101 pp.

CODEN: PIXXD2

DT Patent

LA English

FAN.CNT 5

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
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PI	WO 2001077355	A2	20011018	WO 2001-US11398 20010406
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TI Moss genes from ****Physcomitrella**** ****patens**** encoding proteins involved in the synthesis of carbohydrates

IN Lerchl, Jens; Renz, Andreas; Ehrhardt, Thomas; Reindl, Andreas; Cirpus, Petra; Bischoff, Friedrich; Frank, Markus; Freund, Annette; Duwenig, Elke; Schmidt, Ralf-Michael; Reski, Ralf

PA Basf Plant Science G.m.b.H., Germany

SO PCT Int. Appl., 133 pp.

CODEN: PIXXD2

DT Patent

LA English

FAN.CNT 1

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
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PI	WO 2001044476	A2	20010621	WO 2000-EP12697 20001214
----	---------------	----	----------	--------------------------

From: Collins, Cynthia
Sent: Friday, June 14, 2002 6:07 PM
Subject: STIC-Biotech/ChemLib
sequence search request SN 09/828302

Please search, both prior art and interference, for SN 09/828302:

- 1) SEQ ID NO:9
- 2) SEQ ID NO:14

Thank You,

Cynthia Collins
Art Unit 1638
CM1, 9A12 (office) or 9E12 (mailbox)
(703) 605-1210

FD. 4/6/01 No art
Prov 4/7/00 @ 100%
1026 4/7/99

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if Contact:
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Date Picked Up: _____
Date Completed: 6/21/02
Searcher Prep/Review: _____
Clerical: _____
Online time: _____

TYPE OF SEARCH:
NA Sequences: _____
AA Sequences: _____
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST(where applic.)
STN: _____
DIALOG: _____
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DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: _____
WWW/Internet: _____
Other (specify): _____

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: June 19, 2002, 17:46:14 ; Search time 1689.55 seconds
(without alignments)
10752.509 Million cell updates/sec

Title: US-09-828-302-9
Perfect score: 1346
Sequence: 1 gcgatcatttgcagg.....ccttgccttgatagc 1346

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

EST: *
1: em_estba: *
2: em_esthum: *
3: em_estin: *
4: em_estmu: *
5: em_estov: *
6: em_estpi: *
7: em_estro: *
8: em_htc: *
9: gb_est1: *
10: gb_est2: *
11: gb_htc: *
12: gb_gss: *
13: em_gss_hum: *
14: em_gss_inv: *
15: em_gss_pln: *
16: em_gss_vrt: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	245.6	18.2	799	10	BI405732
2	229	17.0	414	10	BJ196973
3	213.4	15.9	727	10	BG595786
4	205.8	15.3	577	10	BE805365
5	196.8	14.6	520	10	BE556233
6	191.6	14.2	704	10	BI269796
7	189.4	14.1	527	10	BI701028
8	186.2	13.8	497	10	BI701941
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10	182.8	13.6	609	10	BE330853
11	181.6	13.5	493	10	BE941416
12	177.2	13.2	478	9	BE021852
13	175.4	13.0	680	10	BE819859
14	175	13.0	516	10	BI307827
15	171.6	12.7	638	10	BG587548
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18	166	12.3	628	9	AI795639
19	164.6	12.2	666	10	BF635584
20	162.6	12.1	752	10	BG647922
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22	160	11.9	583	9	AI770324
23	159.4	11.8	667	9	AI881291
24	156.8	11.6	556	10	BF632292
25	156.2	11.6	446	9	AUI72997
26	154.4	11.5	582	9	AW146619
27	152.6	11.3	723	10	BE660717
28	151.6	11.3	613	10	BF595352
29	151.4	11.2	519	10	BF008775
30	150.4	11.2	597	9	AW185772
31	150.2	11.2	574	10	BI785332
32	150	11.1	583	9	AW755381
33	150	11.1	635	10	BG238499
34	149.8	11.1	567	10	BM093484
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37	149.8	11.1	579	10	BM093479
38	149.8	11.1	586	10	BI424567
39	149.8	11.1	696	10	BE660711
40	149.4	11.1	545	10	BF598317
41	148.8	11.1	598	10	BG045998
42	148.6	11.0	611	9	AW100049
43	148.2	11.0	513	10	BG509559
44	147.2	10.9	560	10	BF648487
45	147.2	10.9	593	9	AW692843

ALIGNMENTS

RESULT	1	799 bp	mrna	linear	EST 14-AUG-2001
BI405732	115F11 Mature tuber lambda ZAP Solanum tuberosum cDNA, mRNA				
LOCUS	BI405732				
DEFINITION	sequence.				
ACCESSION	BI405732				
VERSION	BI405732.1				
KEYWORDS	EST.				
SOURCE	potato.				
ORGANISM	Solanum tuberosum				
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum.				
AUTHORS	1 (bases 1 to 799)				
TITLE	Nielsen,K.L, Crookshanks,M., Emmersen,J. and Welinder,K.G.				
JOURNAL	EST-sequencing of mature potato tuber (Var. Kuras)				
COMMENT	Unpublished (2000) Contact: Karen G. Welinder Institut for bioteknologi Aalborg Universitet Sohngaardsholmsvej 49, 9000 Aalborg, Denmark Tel: +45 96358467 Fax: +45 98141808 Email: kgw@bio.auc.dk Sequenced from the 5' end. High quality sequence stop: 799 POLYA-No.				
FEATURES	Location/Qualifiers				
source	1..799				
	/organism="Solanum tuberosum"				
	/cultivar="Field grown Kuras"				
	/db_xref="taxon:4113"				
	/clone_lib="Mature tuber lambda ZAP"				
	/tissue_type="tuber"				
	/note="Vector: Lambda ZAP"				
BASE COUNT	236 a	144 c	200 g	219 t	
ORIGIN					
Query Match	18.2%	Score	245.6;	DB	10;
			Length	799;	

AUTHORS van der Hoeven, R., Bezzerides, J., Sun, H., Cho, J., Chierning, A.,
Bongri, O., Buell, C.R., Ronning, C., Tanksley, S. and Baker, B.
TITLE Generations of ESTs from sprouting potato eyes
JOURNAL Unpublished (2000)
COMMENT Contact: Cathy Ronning
The Institute for Genomic Research
For clone info: please contact Research Genetics, Libraries
Division tel 1-800-711-6195, email cdna@resgen.com
FEATURES Seq primer: M3F-R.
Location/Qualifiers
1..727
/organism="Solanum tuberosum"
/cultivar="Kennebec"
/db_xref="taxon:4113"
/clone_lib="CST311F23"
/clone_lib="GSTs"
/tissue_type="sprouting eyes from tubers"
/dev_stage="12-14 weeks post harvest"
/lab_host="SOLR"
/note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2:
XhoI; Various sizes of sprouting eyes (2mm to 15mm) were
taken from tubers. The tubers were incubated at 26C in the
dark for 2-3 weeks prior to sprouting. The eyes were
frozen in liquid nitrogen immediately upon removal from
tubers."
BASE COUNT 222 a 113 c 190 g 202 t
ORIGIN

Query Match 15.9%; Score 213.4; DB 10; Length 727;
Best Local Similarity 59.0%; Pred. No. 2.7e-49;
Matches 443; Conservative 0; Mismatches 271; Indels 37; Gaps 3;

QY 32 agaggatggaattatcttctctccaaagactgacaagacatccgaagatgatgag 91
Db 13 ATAGCAATGGGAACAACTCTCAGCATTCCTAAACTGAAAGTTCTCAGAAGATGGTGA 72

QY 92 aatgcgaggttacgctatggtttatcagccatgcaagggtgctgcgcatagcatgagat 151
Db 73 AATGACATCTAGATATGGTTATCATCTATGCAAGGTGGCGTGCAACATCGAAGAT 132

QY 152 gcacacaagctatctttaaagctgtgataagaacacgtcacaatcaatattggcatcttt 211
Db 133 GCACATGGCGG-----GCATCTTGATGTGGATTCATCCACTTCGTTTTCGGTGTAT 186

QY 212 gatgtcacgaggttaattgtgcaaaattttgtcaagacacttacaccaagagtt 271
Db 187 GATGTCATGAGGTGAGCGGTGCAAGTTTGTGCCAAGCTTCACCAACAGGTG 246

QY 272 ctgaagctgaagcgtacgctaaaggtgacttaaaagcaagtttgggaatttcctttta 331
Db 247 CTCAGAGCTGAAGATACATAGCTGGAGATCTTGGAACTCTCTACGAAAGCATTTTG 306

QY 332 cggatggtgatgatgataaaggagcaagtggtggtggaagacttcaagtttggagaa 391
Db 307 AGAATGGATGATGATCGGTGGTCAAGGGGATGGAGGAAATAGGAGTCTTAGGTGAT 366

QY 392 caaagtacgcttgataaactcgttaagtgaataagctcctcctaatgagagagagat 451
Db 367 AAGGTAAAGGGTTCAATGGAATTAATGAAGATTGATTCGGTCTCCAAGAGCAATGAT 426

QY 452 gacgaaagtattatcctatgctgtcctaactgaaagcaatgatatgaacttggccact 511
Db 427 -----AATAAGGACCAAGATGATGATGGCGCTTT 456

QY 512 aaaaagcataaatttcagatttcagggtccctatttgaggtactgagtggtgct 571
Db 457 GAGAGGGGCTCATTCAGATTTGATGGACCAATTCAGGAACACTGCTGTGTGCA 516

QY 572 ctgattcgtggaataaactgttcgtcgcaaacgtggagactctcgtcgataatgct 631
Db 517 ATCATGAACAACACTACTTTTGTTCGGAATGCTGTGTATTCACGCTCGTAATATCT 576

QY 632 cgacgtggcagagcttaaatctctcgattgatcacaaacccaactagatgagag 691
Db 577 AGAATGGTCAGGCATACAAATTATCTAGAGATCAAAACCTGAGCTTGTGATTGAGAAG 636

QY 692 aaaaagtagagagt-gctggaggtctccatggtgctgttaacggttagtctaaa 750
Db 637 GAAGAATCTATAAGGCTGGTGGTTTATTTCATGACGAGGACCAATTAATGGGAGTTAAA 696

QY 751 tctacaagagcaataggggacatgaattc 781
Db 697 TCTTGCAAGAGCTATAGGTGAGCTGGACTTC 727

RESULT 4
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LOCUS
DEFINITION
ss41q11.y1 Gm-cl061 Glycine max cDNA clone GENOME SYSTEMS CLONE ID:
Gm-cl061-1341 5' similar to TR:Q9SZ53 Q9SZ53 PROTEIN PHOSPHATASE
2C-LIKE PROTEIN. ; mRNA sequence.
ACCESSION
BE805365
VERSION
BE805365.1 GI:10236477
KEYWORDS
EST.
SOURCE
soybean.
ORGANISM
Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
Glycine.
REFERENCE
1 (bases 1 to 577)
Shoemaker, R., Keim, P., Vodkin, L., Erpelting, J., Corvelli, V., Khanna
A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C.,
Wyllie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers
Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk
R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann
R., Waterston, R. and Willson, R.
Public Soybean EST Project
Unpublished (1999)
CONTACT: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available through: Resgen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 35801 For further information
call: (800)-533-4363 or contact via email: ccu@resgen.com
High quality sequence stop: 412.
Location/Qualifiers
1..577
/organism="Glycine max"
/db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-cl061-1341"
/clone_lib="Gm-cl061"
/tissue_type="mature flowers of field grown plants"
/lab_host="DH10B"
/note="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2:
XhoI; The cDNA library was constructed from mRNA isolated
from mature flowers of field grown plants for the cultivar
Raiden. Complementary DNA was synthesized from mRNA using
a primer consisting of a poly(dT) sequence with a XhoI
restriction site. EcoRI adapters were ligated to the
blunt-ended cDNA fragments followed by XhoI digestion. The
cDNA fragments were directionally cloned into the
EcoRI-XhoI restriction site of the pBluescript vector. The
ligated cDNA fragments were transformed into DH10B host
cells (GibcoBRL). This library was constructed in the
laboratory of Dr. Randy Shoemaker."
BASE COUNT 165 a 101 c 143 g 168 t
ORIGIN

Query Match 15.3%; Score 205.8; DB 10; Length 577;


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RESULT 6
BI269796      704 bp      mRNA      linear      EST 18-JUL-2001
LOCUS      NF016C08IR1F1065 Irradiated Medicago truncatula cDNA clone
DEFINITION      NF016C08IR 5', mRNA sequence.
ACCESSION      BI269796
VERSION        BI269796
KEYWORDS       EST.
SOURCE         barrel medic.
ORGANISM       Medicago truncatula
               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
               Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
               Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
               Medicago.
REFERENCE      1 (bases 1 to 704)
AUTHORS        Torres-Jerez,I., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J.,
               Flores,H.R., Inman,J.T., Weller,J.W. and May,G.D.
TITLE          Expressed Sequence Tags from the Samuel Roberts Noble Foundation
               Medicago truncatula irradiated library
JOURNAL        Unpublished (2001)
COMMENT        Contact: May GD
               Plant Biology Division
               The Samuel Roberts Noble Foundation
               2510 Sam Noble Parkway, Ardmore, OK 73402, USA
               Tel: 580 221 7391
               Fax: 580 221 7380
               Email: gdmay@noble.org
               Insert Length: 704 Std Error: 0.00
               Plate: 016 row: C column: 08
               Seq primer: TCACACAGGAACAGCTATGAC.
               Location/Qualifiers
                 1..704
                   /organism="Medicago truncatula"
                   /db_xref="taxon:3880"
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                   /tissue_type="seedlings"
                   /dev_stage="seedling"
                   /note="Vector: Lambda Zap; Seedlings were exposed either
                   to 100 Gy gamma or 0.5, 1, 5, or 10 kJ/m2 UV irradiation.
                   Gamma-irradiated samples were harvested at 6, 12, 24 and
                   48 hours after treatment. UV-irradiated samples were
                   harvested 24 hours post-treatment. cDNA was prepared from
                   polyA+ enriched, pooled samples of equivalent amounts of
                   total RNA from each sample. The cDNA was directionally
                   ligated into the Uni-Zap XR vector (Stratagene) and
                   packaged using the Gigapack III Gold packaging extracts.
                   Phagemids containing cDNA inserts were in vivo excised
                   from the recombinant Uni-Zap XR vector using ExAssist
                   helper phage and the E. coli strain XL1-Blue MRF'
                   (Stratagene). Excised plasmids were plated using SOLR
                   cells."
BASE COUNT      189 a 121 c 193 g 197 t      4 others
ORIGIN
Query Match      14.2%; Score 191.6; DB 10; Length 704;
Best Local Similarity 59.5%; Pred. No. 3.9e-43;
Matches 356; Conservative 0; Mismatches 238; Indels 4; Gaps 2;

QY 499 taacttgccataaaagcataataattccagattccagggtccattatggagtagc 558
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DB 88 TGAGTGGGCTTTTGGAGGAGGACCCCATTCGATTTCAGTGGCCCTAACTGTGGAAGCAC 147
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QY 559 tgcagtgggtctgattcgtggcaataaactgtctcgaactgagactctcg 618
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DB 148 GCGGTGTGGGTGTCATCAGAGGAACAACACTTGTTCGAATGCTGTGATTCTAG 207
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 619 ctgcataatgtctgacgtggcgaggtgtgtaactctcgtattgatacaaacccacct 678
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DB 208 ATGTGTGTTATCAAGAAAGGCCAGGCACACAATTTGCTAAAGATCACAGCCTGATCT 267
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 679 agagcatgagagaaaggatagagagtgtcgtggaggtctcctcatggtggtgtgtaa 738
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Db 268 TGAGTTGAGAAGACAGGATTCTAAAGCTGCGGTTTCATCCAAAGTTGGACAGTCAA 327
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Db 388 GCCTGCTGAAAAGCAGGTTTGTGATCTGCTGACGTGACGTAACTTCGGTTGAGCTTTGCAA 447
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Db 448 AGATGATGAGTTCTTGTGATAGCTTGTGATGGGATATGGGATTCGATGTCAGCCAGC 507
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Db 508 AGCTTGTGGACTTCATACATGCCAGTTAAAGACGGAGAATAAACTTTCTGTGTTTGTG 567
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Db 568 ANAAGTATTTCNATAGTGTCTTGGCACCAACAGCTGG---TGTGAGGGATGTGATAACA 624
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QY 1038 tgagcatcattatagtcacacaaagcaatcgggagtgtgcagcatctcttccacaga 1095
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Db 625 TGACCATGATCTTGATTCANTTCAAAATCCTCTGACTTCANATGCTTCTGTGCACAGA 682
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RESULT 7
BI701028      527 bp      mRNA      linear      EST 29-NOV-2001
LOCUS      sag54a02.v1 Gm-cl082 Glycine max cDNA clone GENOME SYSTEMS CLONE
DEFINITION      ID: Gm-cl082-28 5' similar to TR:Q9SZ53 Q9SZ53 PROTEIN PHOSPHATASE
               2C-LIKE PROTEIN. ;, mRNA sequence.
ACCESSION      BI701028
VERSION        BI701028
KEYWORDS       EST.
SOURCE         soybean.
ORGANISM       Glycine max
               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
               Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
               Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
               Glycine.
REFERENCE      1 (bases 1 to 527)
AUTHORS        Shoemaker,R., Kelm,P., Vodkin,L., Erpelting,J., Corvett,V., Khanna
               ,A., Bolla,B., Marra,M., Hillier,L., Kucaba,F., Martin,J., Beck,C.,
               Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers
               ,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk
               ,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann
               ,R., Waterston,R. and Willson,R.
               Public Soybean EST Project
               Unpublished (1999)
               Contact: Shoemaker R/Public Soybean EST Project
               Public Soybean EST Project
               Washington University School of Medicine
               4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
               Tel: 314 286 1800
               Fax: 314 286 1810
               Email: est@watson.wustl.edu
               This clone is available through: ResGen, Invitrogen Corp. 2130
               South Memorial Parkway Huntville, AL 35801 For further information
               call: (800)-533-4363 or contact via email: ccu@resgen.com
               Seq primer: -40RP from Gibco
               High quality sequence stop: 421.
               Location/Qualifiers
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                   /db_xref="taxon:3847"
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                   /clone_lib="Gm-cl082"
                   /tissue_type="Roots of bulked Minsoy x Noir RI progeny"
                   /lab_host="DH10B"
                   /note="Vector: pBluescript II SK+; Site_1: EcoRI; Site_2:

```


COMMENT

Contact: Michael A. Grusak
USDA/ARS Children's Nutrition Research Center
Baylor College of Medicine
1100 Bates Street, Houston, TX 77030-2600, USA
Tel: 713-798-7044
Fax: 713-798-7078
Email: mgrusak@bcm.tmc.edu
B394682e
TIGR sequence name: MTOAA05TK
More information is available at: www.medicago.org
Seq primer: SKmod (CTA GAA CTA gta gAT CC).
Location/Qualifiers

FEATURES

source

1..516
/organism="Medicago truncatula"
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/db_xref="taxon:3880"
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/tissue_type="immature pod walls"
/dev_stage="immature pods, ranging in age from 15 to 30 days after pollination"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI; Immature pods, ranging in age from 15 to 30 days after pollination, were collected from greenhouse-grown plants. At harvest, seeds were removed from pods and isolated pod walls were collected and immediately frozen in liquid nitrogen. Pod walls were pooled for mRNA extraction. cDNA was prepared from polyA+ enriched RNA. The cDNA was directionally ligated into the Unizap XR vector from Stratagene and packaged using Gigapack III Gold packaging extracts. Plasmids containing cDNA inserts were excised from the recombinant lambda-Zap phage using Ex-assist helper phage and propagated in XL0LR cells."
BASE COUNT 139 a 88 c 148 g 141 t
ORIGIN

Query Match 13.0%; Score 175; DB 10; Length 516;
Best Local Similarity 60.3%; Pred. No. 1.7e-38;
Matches 289; Conservative 0; Mismatches 150; Indels 0; Gaps 0;

QY 499 taacttggccataaaagacataattatccagattccagggtccattatggagtagtac 558
DB 38 TGAGTGGGCTTTGAGGAGGACCCCATCTGATTTCAAGTGGGGCTAACTGGAAGC 97
QY 559 tgcagtggtgctgctgctgctgctgctgctgctgctgctgctgctgctgctgct 618
DB 98 GCGGTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 157
QY 619 ctgcataatgtctgacgtggtggtggtggtggtggtggtggtggtggtggtggtggt 678
DB 158 ATGTGTGTATCAAGGAAAGGCGGACGACACAAATTTGTCTAAGATCAAGCCTGATCT 217
QY 679 agagcatgagagaaagatagagctgctgagctgctgctgctgctgctgctgctgctgct 738
DB 218 TGAGGTGGAAGACAGAGAGTCTTAAGCTGGCGGTTTCATCCAGTTGGACGAGTCAA 277
QY 739 cgtgtactataatcttaccagagcaataggggacatgaattcaaggtgcacctgattt 798
DB 278 TGGAACTTTGAATTTGGCTTAGAGCAATTTGGAGATATGGAATCAAGCAGAACAGTATT 337
QY 799 gccacctgacaagcaagttagtgaactgtgtcccgatgtgttgcgaagtgcacctggacc 858
DB 338 GCGTGTGAAAAGCAGGTGTGACCTGCTGATCCCTGACCTAACCTCCGTTGAGCTTTGCAA 397
QY 859 cggggatgaatttatgtctgctgctgctgctgctgctgctgctgctgctgctgctgctgct 918
DB 398 AGATGATGAGTCTTGTGATGAGCTGTGATGGGATATGGGATATGATGATGATGATGAT 457
QY 919 tgcgtggactctgtttaataatcaagattaccctaccaccaccaccaccaccaccaccacc 977
DB 458 GCTTGTGGACTTCATACATGGCCAGTTAAAGACGGAAGATAAATCTTCTGTGGTTGTG 516

RESULT 15

BG587548
LOCUS
DEFINITION
EST489311 MHAM Medicago truncatula/Glomus versiforme mixed EST
Library cDNA clone pMHAM-50G24 5' end, mRNA sequence.
ACCESSION
BG587548
VERSION
BG587548.1 GI:13602603
KEYWORDS
EST.
SOURCE
Medicago truncatula/Glomus versiforme mixed EST library.
ORGANISM
Medicago truncatula/Glomus versiforme mixed EST library.
REFERENCE
1 (bases 1 to 638)
AUTHORS
Harrison, M.J., Liu, J., Town, C.D., Van Aken, S., Utterback, T., Cho, J. and Fraser, C.M.
TITLE
ESTs from roots of Medicago truncatula after colonization with Glomus versiforme, 2001
JOURNAL
Unpublished (2001)
COMMENT
Contact: Harrison M.J.
Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73401
Tel: 580-223-5810
Fax: 580-221-7380
Email: mjharrison@noble.org
Noble EST name: N386609e TIGR sequence name: MTDDH48TK More information is available at: http://www.medicago.org
Seq primer: SKmod (CTA GAA CTA gta gAT CC).
Location/Qualifiers
1..638
/organism="Medicago truncatula/Glomus versiforme mixed EST library"
/cultivar="Medicago truncatula genotype A17"
/db_xref="taxon:119092"
/clone="pMHAM-50G24"
/clone_lib="MHAM"

FEATURES

source

1..638
/organism="Medicago truncatula/Glomus versiforme mixed EST library"
/cultivar="Medicago truncatula genotype A17"
/db_xref="taxon:119092"
/clone="pMHAM-50G24"
/clone_lib="MHAM"
/tissue_type="roots colonized with Glomus versiforme"
/dev_stage="Roots harvested at 10, 17, 22, 31 and 38 days post-inoculation with Glomus versiforme. The library was made from a mixture of RNA from each of these stages."
/lab_host="E. coli strain XL0LR"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI; cDNA was prepared from polyA+ enriched RNA from roots harvested at 10, 17, 22, 31 and 38 days post-inoculation with Glomus versiforme. The cDNA was directionally ligated into the Unizap XR vector from Stratagene and packaged using Gigapack III Gold packaging extracts. Plasmids containing cDNA inserts were excised from the recombinant lambda-Zap phage using Ex-assist helper phage and propagated in XL0LR cells."
BASE COUNT 194 a 98 c 168 g 178 t
ORIGIN

Query Match 12.7%; Score 171.6; DB 10; Length 638;
Best Local Similarity 57.4%; Pred. No. 1.7e-37;
Matches 371; Conservative 0; Mismatches 239; Indels 36; Gaps 2;

QY 54 gctctcaagactgacacagacatccgaagatgtagagatccgagttacgtctggtt 113
DB 1 GCATTCCTTAAGCTGAAGATCTCAGAGATGGTGAATGCAATCTTAGATATGTT 60
QY 114 tatcagccatgcaagggtggtgcgcgtagatgtaggagtagcacacaagaactatcttaaacg 173
DB 61 TATCATCTATGTAAGGTGGCGTGCACCAATGAAGATGCATCATCGGG- - - - -GCATC 114
QY 174 ttgataagaacacgtcaacatcaatttggcatcttggatggtcacagagtagaatgg 233
DB 115 TTGATGTGATTCATCCACTTCGTTTCGGTGTATATGATGTTGTGATGAGTAGGCGG 174
QY 234 tggcaaaaattgtgcaaaagcacttacaccaagaggttctgaagtcgaagcgtacgcta 293
DB 175 TTGCAAAAGTTTGTGCGCAAGCACCTTCACCAACAGGTGCTCAAGAGTGAAGATACATAG 234

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 19, 2002, 18:42:44 ; Search time 53.31 Seconds
(without alignments)
6201.889 Million cell updates/sec

Title: US-09-828-302-9
Perfect score: 1346
Sequence: 1 gcgatcgtttgcaagg.....ccttgccttcgatcgc 1346

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents_NA.*
1: /cgn2.6/ptodata/1/ina/5A_COMB.seq.*
2: /cgn2.6/ptodata/1/ina/5B_COMB.seq.*
3: /cgn2.6/ptodata/1/ina/6A_COMB.seq.*
4: /cgn2.6/ptodata/1/ina/6B_COMB.seq.*
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6: /cgn2.6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	127.8	9.5	1890	3	US-08-935-855-19
2	120	8.9	1824	2	US-08-822-701-1
3	120	8.9	1824	3	US-08-935-855-1
4	120	8.9	2081	3	US-08-935-855-21
5	99.6	7.4	2268	2	US-08-873-093-2
6	55.8	4.1	7218	1	US-08-232-463-14
7	50.2	3.7	1403	3	US-09-013-881-10
8	36.4	2.7	2750	3	US-08-617-860B-33
9	35	2.6	289	4	US-09-007-005-17
10	35	2.6	289	4	US-09-244-796-17
11	33.6	2.5	12047	2	US-09-022-461-1
12	32.8	2.4	2277	1	US-08-676-967-2
13	32.8	2.4	2277	1	US-08-676-974-2
14	32.8	2.4	2277	2	US-09-098-487-2
15	32	2.4	1498	1	US-08-118-469A-1
16	32	2.4	1498	1	US-08-909-119-1
17	32	2.4	3186	1	US-07-688-352C-23
18	32	2.4	3186	2	US-08-474-379C-23
19	32	2.4	3186	3	US-09-146-249A-23
20	32	2.4	3186	3	US-08-206-188B-23
21	32	2.4	3186	5	PCT-US91-02714-22
22	32	2.4	3890	2	US-08-942-521B-1
23	32	2.4	3890	3	US-09-192-702-1
24	32	2.4	3890	4	US-08-445-474-1
25	32	2.4	3890	5	PCT-US94-02612-1
26	32	2.4	4068	2	US-08-474-379C-58
27	32	2.4	4068	3	US-09-146-249A-58

28	32	2.4	4068	3	US-08-206-188B-58	Sequence 58, Appl
29	31.8	2.4	3918	4	US-08-936-165A-243	Sequence 243, App
30	31.8	2.4	8959	1	US-08-920-812-1	Sequence 1, Appli
31	31.8	2.4	8959	1	US-08-920-827-1	Sequence 1, Appli
32	31.8	2.4	8959	1	US-08-921-177-1	Sequence 1, Appli
33	31.8	2.4	8959	1	US-08-362-577C-1	Sequence 1, Appli
34	31.8	2.4	8959	2	US-08-920-828-1	Sequence 1, Appli
35	31.6	2.3	3635	2	US-08-553-436A-5	Sequence 5, Appli
36	31.4	2.3	3539	4	US-08-853-948B-1	Sequence 1, Appli
37	31.4	2.3	8920	4	US-08-446-855A-1	Sequence 1, Appli
38	31.4	2.3	8920	4	US-09-150-741-1	Sequence 1, Appli
39	31.2	2.3	867	2	US-08-466-103A-5	Sequence 5, Appli
40	30.8	2.3	1988	1	US-08-469-202-26	Sequence 26, Appli
41	30.8	2.3	1988	2	US-08-484-434C-33	Sequence 33, Appli
42	30.8	2.3	2000	1	US-08-469-202-25	Sequence 25, Appli
43	30.8	2.3	2000	2	US-08-484-434C-32	Sequence 32, Appli
44	30.4	2.3	312	4	US-09-191-852-20	Sequence 20, Appli
45	30.4	2.3	312	5	PCT-US95-13376-20	Sequence 20, Appli

ALIGNMENTS

RESULT 1
US-08-935-855-19
; Sequence 19, Application US/08935855
; Patent No. 6056485
; GENERAL INFORMATION:
; APPLICANT: Guthridge, Mark
; APPLICANT: Basilico, Claudio
; TITLE OF INVENTION: NOVEL GROWTH FACTOR INDUCIBLE
; TITLE OF INVENTION: SERINE/THREONINE PHOSPHATASE, FIN13
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; STREET: Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/935,855
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 1049-1-002 CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 1890 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens

US-08-935-855-19
Query Match 9.5%; Score 127.8; DB 3; Length 1890;
Best Local Similarity 59.5%; Pred. No. 1.4e-31;
Matches 235; Conservative 0; Mismatches 157; Indels 3; Gaps 1;

; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-935-855-1

Query Match 8.9%; Score 120; DB 3; Length 1824;
Best Local Similarity 57.2%; Pred. No. 4.8e-29;
Matches 238; Conservative 0; Mismatches 175; Indels 3; Gaps 1;

Qy 529 agattccagggtcccatattatgggagtagctgcagtggtggctctgattcgtgggcaataa 588
Db 714 AGAAGAGCCTGGTTCTGACAGTGGCACAACAGCGGTGGTGGCTCTGATCAGAGGGAAGCA 773
Qy 589 actgttcgtcgaacacgtgagactctgcataaagtctcgcagctggtggcgaggtgt 648
Db 774 GTTGATGTGGCCCAATGCAGAGACTCTCGCTGTGTGGTGTCCGAGGCTGGCAAAAGCTTT 833
Qy 649 aaatctctcagattgatcacaaacccacctagagcatgagagagaaagatagagagtc 708
Db 834 AGATATGTCCTATGACCACAACACAGAGGATGAAGTGGAGCTGGCACGCATCAAGAATGC 893
Qy 709 tggagggc---ttcgtccatggtggtcgtttaacggtagctctaaatcttacaagagcaat 765
Db 894 TGGTGGCAAGTACCATGATGAGCAGAGTCAATGGAGGCTCAACCTCTCCAGGGCCCAT 953
Qy 766 aggggacatggaattcaagggtgcacctgattggccacctgacaagcaagtagtagtcg 825
Db 954 TGGAGACCATCTTACAAAGAGAAACAAAACCTTGGCCACCCAGGAACAGATGATTTCTGC 1013
Qy 826 ctgtcccgatgtgtcgaagtgcacctgggacccggggatgaatttatcgtctggcctg 885
Db 1014 CCTTCTGACATCAAGTGCTGACTCTCACTGATGACCATGAATTCATGGTCATTGCTTG 1073
Qy 886 tgatggaatatgggatgttattgtctagtcagctgctcgtggacctcgtttaaatacaa 941
Db 1074 TGACGGCATCTGGAATGTGATGAGCAGCCAGGAGGTGTGATAGACTTTATTCAATCAA 1129

RESULT 4
US-08-935-855-21
; Sequence 21, Application US/08935855
; Patent No. 6066485
; GENERAL INFORMATION:
; APPLICANT: Guthridge, Mark
; APPLICANT: Basilio, Claudio
; TITLE OF INVENTION: NOVEL GROWTH FACTOR INDUCIBLE
; TITLE OF INVENTION: SERINE/THREONINE PHOSPHATASE, FIN13
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/935,855
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 1049-1-002 CIP

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2081 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Mus musculus
US-08-935-855-21

Query Match 8.9%; Score 120; DB 3; Length 2081;
Best Local Similarity 57.2%; Pred. No. 5.2e-29;
Matches 238; Conservative 0; Mismatches 175; Indels 3; Gaps 1;
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Qy 589 actgttcgtcgaacacgtgagactctgcataaagtctcgcagctggtggcgaggtgt 648
Db 1031 GTTGATGTGGCCCAATGCAGAGACTCTCGCTGTGTGGTGTCCGAGGCTGGCAAAAGCTTT 1090
Qy 649 aaatctctcagattgatcacaaacccacctagagcatgagagagaaagatagagagtc 708
Db 1091 AGATATGTCCTATGACCACAACACAGAGGATGAAGTGGAGCTGGCACGCATCAAGAATGC 1150
Qy 709 tggagggc---ttcgtccatggtggtcgtttaacggtagctctaaatcttacaagagcaat 765
Db 1151 TGGTGGCAAGTACCATGATGAGCAGAGTCAATGGAGGCTCAACCTCTCCAGGGCCCAT 1210
Qy 766 aggggacatggaattcaagggtgcacctgattggccacctgacaagcaagtagtagtcg 825
Db 1211 TGGAGACCATCTTACAAAGAGAAACAAAACCTTGGCCACCCAGGAACAGATGATTTCTGC 1270
Qy 826 ctgtcccgatgtgtcgaagtgcacctgggacccggggatgaatttatcgtctggcctg 885
Db 1271 CCTTCTGACATCAAGTGCTGACTCTCACTGATGACCATGAATTCATGGTCATTGCTTG 1330
Qy 886 tgatggaatatgggatgttattgtctagtcagctcgtcgtggacctcgtttaaatacaa 941
Db 1331 TGACGGCATCTGGAATGTGATGAGCAGCCAGGAGGTGTGATAGACTTTATTCAATCAA 1386

RESULT 5
US-08-873-093-2
; Sequence 2, Application US/08873093
; Patent No. 5853997
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Goli, Surya K.
; APPLICANT: Lal, Preeti
; APPLICANT: Corley, Neil C.
; APPLICANT: Zhang, Hong
; TITLE OF INVENTION: NEW PROTEIN PHOSPHATASE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0

```

: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/873,093
: FILING DATE: Filed Herewith
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER:
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Billings, Lucy J.
: REGISTRATION NUMBER: 36,749
: REFERENCE/DOCKET NUMBER: PP-0319 US
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 415-855-0555
: TELEFAX: 415-845-4166
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 268 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: IMMEDIATE SOURCE:
: LIBRARY: 13177
: CLONE: THPIPLB01
: US-08-873-093-2

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Query Match 7.4%; Score 99.6; DB 2; Length 2268;
Best Local Similarity 51.3%; Pred. NO. 2.5e-22;
Matches 231; Conservative 0; Mismatches 219; Indels 0

QY	550	tgggagtaactcagtggtgctcgtatctcgtgcgaataaaactgctcgcgaacacgctgg	609
DB	457	TGGTTCAACTCGACTGGGAGCTTATGTTTACCTAAGCATATCTACTTTATCAACTGTGG	516
QY	610	agactctgcgtgcataatgctcgcagctgcgcgagctgtaaatctctcgtattgatcaaac	669
DB	517	TGATTCAAGTCTGCTTCTGTATAGGAATGGACAAGTCGCTTTCTACCCAGGATCACAA	576
QY	670	accacaacctagacatgagaggaaagatagagtgctgcgaggtctccatggtgg	729
DB	577	ACCTTTCGAATCCAAGGAAAAGGAGCGAATCCAAAATCAGGAGGACGCGTATGATACA	636
QY	730	tcgtgttaacggtagtctaaatctcaagagcaatagggacatgaaatcaaggtcg	789
DB	637	AGTGTGTTAATGGTTCAATTACAGATATCTCGTCTCTGGGGACTATGATTCAAGGTGT	696
QY	790	acctgatttgcacactgacaagcaagtatgacgtgctgtcccgatgtgtcgaaagtga	849
DB	697	TGATGGCAAGGGCCCAACAGAACACTGTGTTCTCCAGAGCCTCAGGCTTATGAAATTTT	756
QY	850	cccttggaccgggagtaaatatcgtgcgtgcctgtatggaatatggagatttatgctc	909
DB	757	AAGACGACAAGAGGATGAATTTATCATCTTGGCTTGTGATGGGATCTGGGATCTTATGAG	816
QY	910	tagtcaagctcgttgactcgttaaatcaagattacctaaccaccaaaaactctatcctc	969
DB	817	TAATGAGAGCTCTCTGGAATATGTTAAATCAGGCTTCAGGTATCTGATGACCTGGAAA	876
QY	970	tttgtgtgaggagatactggattactgctt	999
DB	877	TGTTGCAATTTGGGTAGTGACACTTGTTT	906

```

RESULT 6
US-08-232-463-14/c
: Sequence 14, Application US/08232463
: Patent No. 5670367
: GENERAL INFORMATION:
: APPLICANT: DORNER, F.
: APPLICANT: SCHEIFLINGER, F.
: APPLICANT: FALKNER, F. G.
: TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
: NUMBER OF SEQUENCES: 52
: CORRESPONDENCE ADDRESS:
:

```

ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMMU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: ptzgpt-Fls
US-08-232-463-14

Query Match 4.1%; Score 55.8; DB 1; Length 7218;
Best Local Similarity 7.8%; pred. No. 1e-07;
Matches 33; Conservative 213; Mismatches 175; Indels 0; Gaps 0;

Qy	218	cacggaagtaaatgtgtggcacaatttttgcagaagcacttacaccaagaaggcttcgaag	277
		: : : : : : : :	
Db	1466	CAAGTAGTTAAAGAGATAGAAGAATTGTGACRRRRRRRRRRRRRRRRRRRRRRR	1407
Qy	278	tctgaacgctcacgtcaaaagtgaacttaaagcaaagtttggaatatctcttttcgcatg	337
		: :	
Db	1406	RRR	1347
Qy	338	gatgatgatgaatgaaggagcaagtgggtggaagagcttcaaagtttgaggagaacaagt	397
		: :	
Db	1346	RRR	1287
Qy	398	agtcagctgtataaacctcgtaatggaaataagctcctctaatacgaggaggatgaacaa	457
		: :	
Db	1286	RRR	1227
Qy	458	agtgattattccctatgctgtgctaaactgaaacaaatgatagtaacttgccactaaaaag	517
		: :	
Db	1226	RRR	1167
Qy	518	cataaatattcagattccagggtcccatttatgggagtagtgcagtggtgctctgatt	577
		: :	
Db	1166	RRR	1107
Qy	578	cgtggcaataaaactgtctgcacaaacctggagactctcgtcgataatgtctcgacgt	637
		: :	
Db	1106	RRR	1047
Qy	638	q 638	


```

; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Translation template
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(289)
; OTHER INFORMATION: n = A,T,C or G
US-09-244-796-17

Query Match      2.6%; Score 35; DB 4; Length 289;
Best Local Similarity 7.3%; pred. No. 0.099;
Matches 17; Conservative 94; Mismatches 122; Indels 0; Gaps 0;

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; Sequence 1, Application US/09022461
; Patent No. 5964371
; GENERAL INFORMATION:
; APPLICANT: HENDERSON, Daniel R.
; APPLICANT: SCHUUR, Eric R.
; APPLICANT: LAMPARSKI, Henry G.
; APPLICANT: YU, De Chao
; TITLE OF INVENTION: PROSTATE CANCER DRUG SCRE
; TITLE OF INVENTION: ENING
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/022,461
; FILING DATE: 12-FEB-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/906,192
; FILING DATE: '04-AUG-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Catherine, Polizzi M
; REGISTRATION NUMBER: 40,130
; REFERENCE/DOCKET NUMBER: 34802-20003.21
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-813-5600
; TELEFAX: 415-494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:

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Thu Jun 20 13:15:33 2002

us-09-828-302-9.rni

Page 9

Search completed: June 19, 2002, 19:49:52
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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: June 19, 2002, 18:43:49 ; Search time 210.22 seconds
(without alignments)
10993.087 Million cell updates/sec

Title: US-09-828-302-9

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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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6	183.4	13.6	787	21	Arabidopsis thalia
7	155.6	11.6	467	21	Zea mays DNA fragm
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9	146	10.8	1824	22	Trichoderma reesei

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11	141.2	10.5	929	21	AAC44093	Zea mays DNA fragm
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18	103.2	7.7	3255	23	ABL04904	Drosophila melanog
19	99.6	7.4	2270	20	AAF05715	Human protein phos
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21	99.2	7.4	2543	21	AAZ97065	Human secreted pro
22	97.8	7.3	1395	20	AAI15662	Protein phosphatas
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33	80.6	6.0	552	20	AAI39627	Breast cancer asso
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KW	protein identification; signal transduction pathway;
KW	metabolic pathway; promoter; termination sequence; ss.
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DT 18-OCT-2000 (first entry)
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KW Protein identification; signal transduction pathway;
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Qy	619	ctgcaataatgtctcgacgtggcgaggtgtgtaaatctctcgtattgatcacaaccaaacct	678	PR	04-MAY-1999;	99US-0132484.
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KW	protein identification; signal transduction pathway;			PR	16-JUN-1999;	99US-0139452.
KW	metabolic pathway; promoter; termination sequence; ss.			PR	17-JUN-1999;	99US-0139453.
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KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.

XX Arabidopsis thaliana.

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KW	protein identification; signal transduction pathway; metabolic;		
KW	pathway; promoter; termination sequence; corn; ss.		
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GenCore version 4.5
Copyright (C) 1993 - 2000 CompuGen Ltd.
OM nucleic - nucleic search, using sw model
Run on: June 19, 2002, 18:11:49 ; Search time 1901.09 Seconds
(without alignments)
14816.299 Million cell updates/sec

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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32: em_htg_other:*

33: em_htgo_inv:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	277.6	20.6	1107	8	AF213455	Zea mays
5	146	10.8	1824	6	AX319337	Sequence
6	129.4	9.6	1919	4	BTU81159	Bos taurus
7	127.8	9.5	1434	6	BC007361	Homo sapi
8	127.8	9.5	1641	6	AX002424	Sequence
9	127.8	9.5	1932	9	HSY13936	Homo sapien
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12	125.6	9.3	486	6	AX341828	Sequence
13	125.6	9.3	492	6	AX351366	Sequence
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17	120	8.9	1824	6	AR083379	S.pombe c
18	120	8.9	2069	10	MMU42383	Mus musculu
19	120	8.9	2181	10	BC009004	Mus muscu
20	115	8.5	3508	3	AF023665	Plasmodiu
21	114.2	8.5	8961	2	AC014563	Drosophill
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27	103.2	7.7	164595	3	AC011907	Drosophill
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30	99.6	7.4	1164	9	AF294792	Homo sapi
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40	97.8	7.3	2250	8	SCUT2498	Saccharomyc
41	97.8	7.3	64797	8	SCE9747	Saccharomyc
42	97.6	7.3	969	3	PTPF2CMR	P.tetraulac
43	94.2	7.0	1673	3	AY051685	Drosophill
44	94	7.0	36162	8	SPAC2G11	S.pombe chr
45	93.2	6.9	68487	2	AC017782	Drosophill

ALIGNMENTS

RESULT	1
LOCUS	AY057611
DEFINITION	Arabidopsis thaliana AT4g31860/F11C18_60 mRNA, complete cds.
ACCESSION	AY057611
VERSION	AY057611.1
KEYWORDS	FLI-CDNA
SOURCE	thale cress.
ORGANISM	Arabidopsis thaliana
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
AUTHORS	1 (bases 1 to 1531) Cheuk, R., Chen, H., Kim, C. J., Koesena, E., Meyers, M. C., Banh, J., Bowser, L., Carinci, P., Dale, J. M., Goldsmith, A. D., Hayashizaki, Y., Ishida, J., Jiang, P. X., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Lam, B., Lee, J. M., Lin, J., Liu, S. X., Miranda, M., Narusaka, M., Nguyen, M., Onodera, C. S., Palm, C. J., Pham, P. K., Quach, H. L., Sakurai, T., Satou, M., Seki, M., Southwick, A., Tang, C. C., Toriumi, M., Yamada, K., Yamamura, Y., Yu, G., Yu, S., Shinozaki, K., Davis, R. W., Theologis, A. and Ecker, J. R.
TITLE	Arabidopsis cDNA clones
JOURNAL	Unpublished

QY	512	aaaaagcataaataatcagatttccagggtcccaatttatgggagtactcagtggtggct	571
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QY	692	aaaagatagagagtgctggaggcttcgtccatcgttggtcgtgttaacggttagtctaatt	751
Db	761	GAAAGGATATTGAAAGCTGGTGGCTTTATTTCACGCTGGGAGAACTCAATGAAAGCTTGAAT	820
QY	752	cttacaagagaataaggagacataagaattcaaggctgcacctgatttgcacctgacaag	811
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DEFINITION	Arabidopsis thaliana putative protein phosphatase 2C		PLN 26-AUG-2001
ACCESSION	AY050873.1		
VERSION	AY050873.1		
KEYWORDS	FLI_CDNA		
SOURCE	Arabidopsis thaliana		
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis		
REFERENCE	1 (bases 1 to 1522)		
AUTHORS	Yamada, K., Liu, S.X., Pham, P.K., Banh, J., Dale, J.M., Goldsmith, A.D., Jiang, P.X., Lee, J.M., Onodera, C.S., Quach, H.L., Tang, C.C., Toriumi, M., Yamamura, Y., Yu, G., Yu, S., Bowser, L., Carninci, P., Chen, H., Cheuk, R., Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Kim, C., Koesema, E., Lam, B., Lin, J., Meyers, M.C., Miranda, M., Narusaka, M., Shinn, P., Southwick, A., Sakurai, T., Satou, M., Seki, M., Shim, P., Southwick, A., Tracy, S.E., Shinohara, K., Davis, R.W., Ecker, J.R. and Theologis, A.		
TITLE	Full Length cDNA of gene F27C12.1/At2g25070 (GI:4559345)		
JOURNAL	Unpublished		
REFERENCE	2 (bases 1 to 1522)		
AUTHORS	Yamada, K., Liu, S.X., Pham, P.K., Banh, J., Dale, J.M., Goldsmith, A.D., Jiang, P.X., Lee, J.M., Onodera, C.S., Quach, H.L., Tang, C.C., Toriumi, M., Yamamura, Y., Yu, G., Yu, S., Bowser, L., Carninci, P., Chen, H., Cheuk, R., Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Kim, C., Koesema, E., Lam, B., Lin, J., Meyers, M.C., Miranda, M., Narusaka, M., Shinn, P., Southwick, A., Tracy, S.E., Shinohara, K., Davis, R.W., Ecker, J.R. and Theologis, A.		

Sakurai,T., Satou,M., Seki,M., Shinn,P., Southwick,A., Tracy,S.E., Shinozaki,K., Davis,R.W., Ecker,J.R. and Theologis,A.
Submitted (24-JUL-2001) Plant Gene Expression Center, 800 Buchanan Street, Albany, CA 94710, USA
RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAs (RAFL cDNA : 'RIKEN Arabidopsis Full-length cDNA'): Seki,M., Narusaka,M., Ishida,J., Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J., Hayashizaki,Y. and Shinozaki,K.

The Salk, Stanford, PGEC (SSP) Consortium members carried out the sequencing and annotation of the RAFL cDNAs: Yamada,K., Liu,S.X., Pham,P.K., Banh,J., Dale,J.M., Goldsmith,A.D., Jiang,P.X., Lee,J.M., Onodera,C.S., Quach,H.L., Tang,C.C., Toriumi,M., Yamamura,Y., Yu,G., Yu,S., Bowser,L., Chen,H., Cheuk,R., Jones,T., Karlin-Neumann,G., Kim,C., Koeseema,E., Lam,B., Lin,J., Meyers,M.C., Miranda,M., Nguyen,M., Palm,C.J., Shinn,P., Southwick,A., Tracy,S.E., Davis,R.W., Ecker,J.R. and Theologis,A.

Yamada,K. (SSP/PGEC) and Seki,M. (RIKEN GSC) contributed equally to this work. Shinozaki,K. (RIKEN GSC) and Theologis,A. (SSP/PGEC) contributed equally to this work as PIs.

FEATURES
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RESULT 4
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LOCUS Zea mays protein phosphatase type-2C (pp2c-1) mRNA, complete cds.
DEFINITION AF213455
ACCESSION AF213455
VERSION AF213455.1 GI:12003989
KEYWORDS Zea mays.
SOURCE Zea mays
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;


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Matches 235; Conservative 0; Mismatches 157; Indels 3; Gaps 1;

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mRNA, complete cds.
ACCESSION
BC022061
VERSION
BC022061.1 GI:18314371
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SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 2169)
Strausberg, R.
Direct Submission
TITLE
Submitted (22-JAN-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA

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REMARK
COMMENT
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/PTP
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology
http://www.systemsbio.org
Contact: anadan@systemsbiology.org
Anup Madan, Jessica Fahey, Erin Helton, Mark Kettman, Anuradha
Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAL Plate: 3 Row: b Column: 21
This clone was selected for full length sequencing because it
passed the following selection criteria: Hexamer frequency ORF
analysis. Location/Qualifiers
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GLNLSRATGDFHYKRNKLPPEEQMISALPDIKVLTLDHDFHFWIACDGLWNYMSQ
EYVDFIQSKISQDENGELRLSIVIELLDQCLAPDTSDDGTGCDNMTICIIICFKPR
NTAELOPSPGKRKLEEVLTSGAEENSGNSDKKAKRD"
BASE COUNT      548 a  545 c  634 g  442 t
ORIGIN

Query Match      9.5%; Score 127.8; DB 9; Length 2169;
Best Local Similarity 59.5%; Pred. No. 1.1e-25;
Matches 235; Conservative 0; Mismatches 157; Indels 3; Gaps 1;

QY 550 tgggagtagcagtggtggtctgattggtggaataaactgttcgcgaaacgctgg 609
Db 1097 TGGTACAACAGCGGTGGTGGCCCTGATACGAGGGAAGCAGTGTGTTAGCAACGCAGG 1156
QY 610 agactctgcgtcataatgtctcgacgtgagcgtgtaaatctctcgatgatcaca 669
Db 1157 AGACTCTCGCTGTGGTATCTGAGGCTGGCAAGCTTTAGACATGCTCTATGATCACA 1216
QY 670 acccaacctagagcatagagagaaagatagagagtgctgagggc---ttcg 726
Db 1217 ACCAGAGGATGAAGTAGAAGTACGACGCTCAAGAAATGCTGTGCAAGGTCACCATGGA 1276
QY 727 tggctgtgtaacggtagctctaaatcttacaagaacatagggacatggaatcaagg 786
Db 1277 TGGCGCAGTCAACGGGGGCTCAACCTCTCCAGAGCCATTGGGACCACTTCTATAAGAG 1336
QY 787 tgcacctgattggccacctgacaagcaagtagtgacgtgctgtcccgatgtgtcgaa 846
Db 1337 AAACAAGAACCTGCCACCTCGAGGACACAGATGATTTTCAGCCCTTCTCTGACATCAAGGTGCT 1396
QY 847 tgaccttgaccgggagatggaattatcgctgctgctgagtgatggaatggttat 906

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Db 1397 GACTCTCACTGACGACCATGAATTCATGCTGATGCGTGTGATGCGATCGAATGTGAT 1456
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Db 1457 GAGCAGCCAGGAAGTTGTAGATTTCATTCATCAATCAA 1491

RESULT 11
LOCUS BC000057
DEFINITION Homo sapiens, 2176 bp mRNA linear PRI 12-JUL-2001
magnesium-dependent, gamma isoform, clone MGC:1675 IMAGE:3505271,
mRNA, complete cds.
ACCESSION BC000057
VERSION BC000057.1 GI:12652622
KEYWORDS MGC.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2176)
Strausberg,R.
Direct Submission
Submitted (03-NOV-2000) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology
http://www.systemsbio.org
contact: amadan@systemsbio.org
Anup Madan, Rachel Dickhoff, Jessica Fahey, Stephanie Ford, Julia
Greene, Mark Kettman and Anuradha Madan

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAL Plate: 7 Row: J Column: 7
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 4505998.
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1. .2176
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/note="Vector: pOTB7"
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/protein_id="AAH00057.1"
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ERGTAGVGPGPTGTEAGDSCSASDKLPVAKSKFFEDSEDESEDEEEDSE
CSEEDGTSSAEANEEDDTEAEDEDEEEMVPMGMEKPEGSDGTAVVA
LIRGKOLIVANAGSRVSVSEAGKALDMSYDHKPEDEVELARIKNAGSKVTMDGRVNG
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551 a 544 c 641 g 440 t

BASE COUNT
ORIGIN

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Query Match 9.5%; Score 127.8; DB 9; Length 2176;
Best Local Similarity 59.5%; Pred. No. 1.1e-25;
Matches 235; Conservative 0; Mismatches 157; Indels 3; Gaps 1;

QY 550 tgggagtaactgcagtggtggtgctgtgattcggtgcaataaactgttcgtcgcaaacgctgg 609
Db 1100 TGGTACAAACAGCGTGTGGCCCTGTACGAGGGAAGCAGTTGATTGTAGCCCAACGACG 1159

QY 610 agactctcgtcgcataatgtctcagctgagcgagctgaaatctctcgatgatcacaa 669
Db 1160 AGACTCTCGCTGTGTGGTATCTCGAGGCTGGCAAGCTTTAGACATGTCCTATGATCACAA 1219

QY 670 acccaacctagacatgagaggaagaaagatagagtgctggaggc---ttcgtccatgg 726
Db 1220 ACCAGAGGATGAAGTAGAAGTAGACGACGATCAAGAATGCTGGTGGCAAGTCAACATGGA 1279

QY 727 tgcgtgttaacggttagtctaaattcttaacagagcaaatagggacatgaattcaagg 786
Db 1280 TGGCGAGTCAACGGGGCCCTCAACCTCTCCAGAGCATTTGGGGACCACTTCTATTAAGAG 1339

QY 787 tcgacctgatttgccacctgacaaagtagtagcgtgctgtcccgatgttgcgaagt 846
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QY 847 tgacctggaccgggagtgaaatttatcgtgctgctgtgaggaataatggatgttat 906
Db 1400 GACTCTCACTGACGACCATGAATTCATGCTGATGCTGATGCGCATCGAATGTGAT 1459

QY 907 gctagtcaagctgctggtgacttcgttaaatcaa 941
Db 1460 GAGCAGCCAGGAAGTTGTAGATTTCATTCATCAATCAA 1494

RESULT 12
LOCUS AX341828
DEFINITION Sequence 2075 from Patent WO0196388.
ACCESSION AX341828
VERSION AX341828.1 GI:18137810
KEYWORDS human.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (sites)
AUTHORS Jiang,Y., Harlocker,S.L. and Secrist,H.
TITLE Compositions and methods for the therapy and diagnosis of colon
cancer
JOURNAL Patent: WO 0196388-A 2075 20-DEC-2001;
CORIXA CORPORATION (US)
FEATURES Location/Qualifiers
source 1..486
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 134 a 111 c 132 g 107 t 2 others
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Query Match 9.3%; Score 125.6; DB 6; Length 486;
Best Local Similarity 59.5%; Pred. No. 4.1e-25;
Matches 231; Conservative 0; Mismatches 154; Indels 3; Gaps 1;

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QY 617 cgtgcataatgtctcagctgagcgaggtgttaactctctcgatgatcacaaacccac 676
Db 64 CGTGTGTGTATCTGAGGCTGGCAAGCTTTAGACATGTCCTATGATCACAAACGACAG 123

QY 677 ctagagcatgagaggaagaaagatagagtgctggaggc---ttcgtccatggtgctgt 733

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Db 124 GATGAAGTAGACTAGCAGCATCAGAAATGCTGTGGCAAGGTCACCATGATGGGCGA 183
QY 734 gttacggttagtctaataattacaagagcaataggggacatggaattcaagggtgacct 793
Db 184 GTCAACGGGGGCGCTCAACCTCCAGAGCATTGGGACCACTTCTCAAGAGAAACAAG 243
QY 794 gatttgcacacctgacaagaagaatagtagcagctgtctcccgatgttgcgaagttgacctt 853
Db 244 AACCTGCCACCTGAGGAACAGATGATTTTCAGCCCTTCCTGCATCAAGGTGCTGACTCTC 303
QY 854 ggaccggggatgaattatctgctggcctgtgatggaatagtgattgttatgtcttagt 913
Db 304 ACTGACGACCAGTAATCATGCTGCTGCTGATGTCGATCGAATGTGATGAGCAGC 363
QY 914 caagctgtcgtgaccttcgtaataca 941
Db 364 CAGGAAGTTGTAGATTTCATTCATCAATCAA 391

RESULT 13
LOCUS AX351366/c
DEFINITION Sequence 113 from Patent WO0196390.
ACCESSION AX351366
VERSION AX351366.1 GI:18616713
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE
AUTHORS Jiang, Y., Hepler, W. T., Clapper, J. D., Wang, A. and Secrist, H.
TITLE Compositions and methods for the therapy and diagnosis of colon
cancer.
JOURNAL Patent: WO 0196390-A 113 20-DEC-2001;
CORIXA CORPORATION (US)
FEATURES
    source      1..492
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                /organism="Homo sapiens"
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ORIGIN

Query Match      9.3%; Score 125.6; DB 6; Length 492;
Best Local Similarity 59.5%; Pred. No. 4.1e-25;
Matches 231; Conservative 0; Mismatches 154; Indels 3; Gaps 1;

QY 557 actgcaagtgtggtctgattcgtggcaataaactgttcgcgaacacgtggagactct 616
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QY 617 cgtcgataatgtctcgcagtcgagcgctgataatctctcgtgattgacatacaaccccaac 676
Db 429 CGCTGTGTGTATCTGAGGCTGGCAAGCTTTAGACATGTCTCTATGATCAACAACCCAGAG 370
QY 677 cttagacatagagagaaaggatagagtgctggaggc---ttcgtccatgggtgctgt 733
Db 369 GATGAAGTAGAAGTACGACGCGATCAAGATGCTGTGTGCAAGGTCACCATGGATGGGCGA 310
QY 734 gttacggttagtctaatacttacaagagcaataggggacatggaattcaagggtgacctt 793
Db 309 GTCAACGGGGGCGCTCAACCTCTCCAGAGCCATTGGGGACCACTTCTCAAGAGAAACAAG 250
QY 794 gatttgcacacctgacaagaagaatagtagcagctgtctcccgatgttgcgaagttgacctt 853
Db 249 AACCTGCCACCTGAGGAACAGATGATTTTCAGCCCTTCCTGCATCAAGGTGCTGACTCTC 190
QY 854 ggaccggggatgaattatctgctggcctgtgatggaatagtgattgttatgtcttagt 913
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QY 914 caagctgtcgtgaccttcgtaataca 941
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DEFINITION Drosophila melanogaster LD27655 full length cDNA.
ACCESSION AY051748
VERSION AY051748.1 GI:15291806
KEYWORDS FLI CDNA.
SOURCE fruit fly.
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 2510)
AUTHORS Stapleton, M., Brokstein, P., Hong, L., Agbayani, A., Carlson, J.,
Champe, M., Chavez, C., Dorsett, V., Farfan, D., Frise, E., George, R.,
Gonzalez, M., Guarin, H., Li, P., Liao, G., Miranda, A., Mungall, C. J.,
Nunoo, J., Pacleb, J., Paragas, V., Park, S., Phouanavong, S., Wan, K.,
Yu, C., Lewis, S. E., Rubin, G. M. and Celniker, S.
Direct Submission
Submitted (10-AUG-2001) Berkeley Drosophila Genome Project,
Lawrence Berkeley National Laboratory, One Cyclotron Road,
Berkeley, CA 94720, USA
Sequence submitted by:
Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory
Berkeley, CA 94720
This clone was sequenced as part of a high-throughput process to
sequence clones from Drosophila Gene Collection 1 (Rubin et al.,
Science 2000). The sequence has been subjected to integrity checks
for sequence accuracy, presence of a polyA tail and contiguity
within 100 kb in the genome. Thus we believe the sequence to
reflect accurately this particular cDNA clone. However, there are
artifacts associated with the generation of cDNA clones that may
have not been detected in our initial analyses such as internal
priming, priming from contaminating genomic DNA, retained introns
due to reverse transcription of unspliced precursor RNAs, and
reverse transcriptase errors that result in single base changes.
For further information about this sequence, including its location
and relationship to other sequences, please visit our Web site
(http://fruitfly.berkeley.edu) or send email to
cdna@fruitfly.berkeley.edu.
FEATURES
    Location/Qualifiers
    1..2510
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        /strain="y; cn bw.sp"
        /db_xref="taxon:7227"
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ORIGIN

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Best Local Similarity 55.1%; Pred. No. 9.1e-25;
Matches 288; Conservative 0; Mismatches 22; Indels 6; Gaps 2;
QY 550 tggagtagctgagtgctgcttaattcgttgccaaataaactgttcgcgaacacgtgg 609
Db 1422 TGGATGACTGCGAGTTGTATGTGTGTGTCGAGGTCGGACCTTTACGTGGCAACGAGG 1481
QY 610 agactcgtcgtcaataatctcgcagctgagcagctgttaaatctcgtcgtgacacaa 669
Db 1482 GGACTCGCGATGTTATATACGCGAGTGGCAAGCCATTGAAATGAGCATCGACCACAA 1541
QY 670 accaaccctagacatga---gaggaagagtagagagtgctgagagcttcgtccatgg 726
Db 1542 GCCCGAAGATGACGAAGACCTCGCGCATATAAAGGCGAGTGTGCGGGTTACACTTGA 1601
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Db 1602 TGGACGCGTAATGAGGCGCTTAATTGTCTCGAGGCCCTTGAGACCATGCTATATAAC 1661
QY 787 tcgacctgatttgcacacctgacaagcaagtagtgacgtgctgtcccgatgttgcgaagt 846
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QY 907 gctagtagaagctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgct 966
Db 1782 GTCTAGTGAGAAAGTTGTAGAAATTTGACGTTGCAGACTAAAGATACAAAATAATTGTC 1841
QY 967 atcttctgtgagagagatactgactgctgctgctgctgctgctgctgctgctgctgct 1023
Db 1842 AACGATTTGAGAGACTTTTGTATACCTTTAGCTCGAATACAAATGGGTGATGGGAC 1901
QY 1024 agagtgataacatgagacatcattatagtcacacacacacacacacacacacacac 1066
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RESULT 15

YSPPP2A YSPPP2A 1920 bp DNA linear PLN 24-MAY-1995
LOCUS Schizosaccharomyces pombe protein phosphatase 2C gene (ptc2+),
DEFINITION complete cds.
ACCESSION L34881
VERSION L34881.1 GI:609655
KEYWORDS protein phosphatase 2C.
SOURCE Schizosaccharomyces pombe (strain 972) DNA.
ORGANISM Schizosaccharomyces pombe
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
Schizosaccharomycetes.
REFERENCE 1 (bases 1 to 1920)
AUTHORS Shiozaki, K. and Russell, P.
TITLE Counteractive roles of protein phosphatase 2C (PP2C) and a MAP
kinase kinase homolog in the osmoregulation of fission yeast
JOURNAL EMBO J. 14 (3), 492-502 (1995)
MEDLINE 95163582
FEATURES Location/Qualifiers
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CDS

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ORIGIN

Query Match 9.0%; Score 121.6; DB 8; Length 1920;
Best Local Similarity 56.9%; Pred. No. 6.6e-24;
Matches 223; Conservative 0; Mismatches 169; Indels 0; Gaps 0;
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QY 659 attgatcacaaaccccaacctagacatgagaggaagagatagagagctgagagcttc 718
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Db 1123 ATCGACTTTGGTGGAGTGAATGGTAGTTTGGCTCTTTCTCGTCCATTTGGAGACTTTGAG 1182
QY 779 ttcaagggtcgacctgatttgcacctgacaagcaagtagtagtgcgtgctcccatgtt 838
Db 1183 TACAAGAAAGACAGTTCCTTACCTCCAGAAAACAGATGTTACAGCTTTTCTCTGATGTC 1242
QY 839 gtccgaagttgacctggaccggggatgaatttatctgtgctgctgctgctgaggaatagg 898
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QY 899 gatgttatgcttagcaagctgctggtgacttcgttaaatcaagattaccctaccacaaa 958
Db 1303 GATTGCAAGAGCTCTCAACAAGTCGTGGAGTTGTGAAGAGAGGCATTGTTCCGCGGCAG 1362
QY 959 actctatcatctttgtgtgagagagatactgga 990
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Search completed: June 19, 2002, 19:48:36
Job time: 5807 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 19, 2002, 08:43:46 ; Search time 28.56 Seconds
(without alignments)
2138.208 Million cell updates/sec

Title: US-09-828-302-14
Perfect score: 1836
Sequence: 1 MGILYCSFKTDKTSDDENA.....MSIIIVQKSGVAASSTD 353

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 17994929 residues
Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_19.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phage.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_rvivirus.*
16: sp_bacteriap.*
17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	973	53.0	357	10 Q9S253	Q9sz53 arabidopsis
3	967	52.7	355	10 O81716	O81716 arabidopsis
4	655.5	35.7	662	5 Q9V9F7	Q9v9f7 drosophila
5	558.5	30.4	371	5 Q9VZS1	Q9vzs1 drosophila
6	552.5	30.1	352	5 Q9WQ00	Q9wq00 drosophila
7	549	29.9	367	5 Q9VBF9	Q9vbf9 drosophila
8	545	29.7	280	5 Q9GPF5	Q9gpu5 sterkiella
9	540.5	29.4	368	5 Q9VAK1	Q9vak1 drosophila
10	540.5	29.4	374	5 Q961C5	Q961c5 drosophila
11	539	29.4	477	11 Q99NF7	Q99nf7 mus musculus
12	538	29.3	387	4 Q9HAY8	Q9hay8 homo sapien
13	534	29.1	465	11 Q99ND8	Q99nd8 rattus norv
14	519	28.3	323	11 Q9E0E2	Q9eqe2 mus musculus
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17	486	26.5	336	4 Q96IN7	Q96in7 homo sapien
18	484.5	26.4	322	5 Q9U5F4	Q9u5f4 entamoeba h
19	457	24.9	920	5 Q43966	Q43966 plasmodium
20	445.5	24.3	341	5 Q9NB46	Q9nb46 caenorhabdi
21	434	23.6	404	5 Q95YR8	Q95yr8 leishmania
22	415.5	22.6	380	10 P93006	P93006 arabidopsis
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27	372.5	20.3	297	6 Q95JY9	Q95jj9 macaca fasc
28	370.5	20.2	392	4 Q9H0C8	Q9h0c8 homo sapien
29	363.5	19.8	442	10 Q9LWV3	Q9lhw3 arabidopsis
30	363	19.8	377	10 Q9LNF4	Q9lnf4 arabidopsis
31	363	19.8	379	10 Q94BM8	Q94bm8 arabidopsis
32	360.5	19.6	392	11 Q92126	Q92126 rattus norv
33	358	19.5	348	10 Q9LEW5	Q9lew5 arabidopsis
34	357	19.4	362	10 Q9ZW21	Q9zw21 arabidopsis
35	355.5	19.4	305	10 Q942N4	Q942n4 oryza sativ
36	355	19.3	511	10 O81709	O81709 arabidopsis
37	355	19.3	511	10 Q9CAJ0	Q9caj0 arabidopsis
38	354.5	19.3	359	10 O82469	O82469 mesembryant
39	354	19.3	434	10 Q43717	Q43717 arabidopsis
40	354	19.3	434	10 Q94C87	Q94c87 arabidopsis
41	354	19.3	854	5 Q9ND28	Q9nd28 leishmania
42	353.5	19.3	396	10 O80871	O80871 arabidopsis
43	351.5	19.1	413	10 Q9FIF5	Q9fif5 arabidopsis
44	351.5	19.1	413	10 Q94417	Q94417 arabidopsis
45	351	19.1	416	10 Q9FLI3	Q9fli3 arabidopsis

ALIGNMENTS

RESULT 1

ID Q9FQY2 PRELIMINARY; PRT; 366 AA.
AC Q9FQY2;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE PROTEIN PHOSPHATASE TYPE-2C.
GN PP2C-1.
OS zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
OC Panicoidae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RP SEQUENCE FROM N.A.
RA Broz A.K., Thelen J.J., Miernyk J.A., Muszynski M.G., Randall D.D.;
RT "ZnPP2, a novel type-2C protein phosphatase from maize.";
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF213455; AAG43835.1; -.
DR HSSP; P35813; 1A6Q.
DR InterPro; IPR001932; PP2C_domain.
DR Pfam; PF00481; PP2C; 2.
DR SMART; SM00332; PP2C; 1.
DR SMART; SM00331; PP2C_SIG; 1.
SQ SEQUENCE 366 AA; 40172 MW; B3C965014EAB6487 CRC64;

Query Match 54.0%; Score 992; DB 10; Length 366;
Best Local Similarity 54.6%; Pred. No. 6.le-72;
Matches 196; Conservative 61; Mismatches 78; Indels 24; Gaps 3;
QY 1 MGILYCSFKTDKTSDDENAELRYGLSAMQWRSDMEDAHKAILNVKNTSTISFGIFDG 60
Db 1 MVILYLPKTKVSGEDGENDKLFGLSSMQWRATMEDAHSLDLNDNTAS--FGVFDG 58
QY 61 HGGKLVAKFCAKHLHQEVLYKSEAYAKGDLKASLEYSFTLRMDMMKGASGWELOSLEPTS 120
Db 59 HGGKLVAKFCAKYLHREYLHTEAYAGDLGAHVHRAVLRMDMMRGRGWRGRELQALGDKI 118


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Qy 135 -----AREDE-----SDYSYAVLTESDNLAT----- 158
Db 239 SNTTTSINDLSTKNAALKDDSVNDQNEGSDTKHTLVSSNNKKLFATGSDNMTLNQS 298
Qy 159 KKHXY-----SDFQ----- 167
Db 299 SKNEFTNSTSKPERFNINSSQDDEFTDDADYBENDNVKSPDTSSAESDCTENDDDGD 358
Qy 168 -----GPIYGSTAVVALIRGNKLFVANAGDSRCIM 197
Db 359 EDGNEDEEETEDQANDNFNCANMIEEPKDSCTAVVCLLQGRDLIYVANAGDSRCVI 418
Qy 198 SRGEAVNLSDHKPNLEHERKRIESAGGVH-GGRVNGSLNLTATGDMFEKGRPLDP 256
Db 419 SRSGQATIESIDHKPEDEDEASRIKAGGRVTLDRGVNGGLNLSRALGDHAYKTNVTLPA 478
Qy 257 DKQVVTCPDVVEVDLPGDFEIVLACDGIWDMVSSQAVDFVKSRLPTTKTTLSSICEEI 316
Db 479 EQMISALPDITKKLIITPEDEFVVLACDGIWNVMSSEVFEVRCRLKDNKKLSTICEEL 538
Qy 317 LDYCLSPTR-QOEGCDNMSSIIIVQPK-----QSGVAASSTSD 353
Db 539 FDNCLAPNTMGDTGCDNMVAVIQEFKKLQELQSTIPPQNOTED 582
Qy 371 LDYCLSPTR-QOEGCDNMSSIIIVQPK-----QSGVAASSTSD 353
Db 539 FDNCLAPNTMGDTGCDNMVAVIQEFKKLQELQSTIPPQNOTED 582
RESULT 5
Q9VZS1 ID Q9VZS1 PRELIMINARY; PRT; 371 AA.
AC Q9VZS1
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-OCT-2001 (TReMBLrel. 18, Last annotation update)
DE CG17746 PROTEIN.
GN CG17746
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_Taxid=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY.
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Vandeil M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jallali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Smith H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
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RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassaman D.A., Weinstock G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-P., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
DR EMBL; AE003477; AAF47746.1; -.
DR HSSP; P35813; IAG0.
DR FlyBase; FBgn0035425; CGI17746.
DR InterPro; IPR000222; PP2C.
DR InterPro; IPR001932; PP2C_domain.
DR Pfam; PF00481; PP2C; 1.
DR SMART; SM00332; PP2Cc; 1.
DR SMART; SM00331; PP2C-SIG; 1.
DR PROSITE; PS01032; PP2C; 1.
SQ SEQUENCE 371 AA; 41009 MW; E45A512772C2E36D CRC64;
Query Match 30.4%; Score 558.5; DB 5; Length 371;
Best Local Similarity 37.6%; Pred. No. 5.8e-37;
Matches 128; Conservative 50; Mismatches 103; Indels 59; Gaps 5;
Qy 1 MGIYLCSPKTDKTSDEENAEIYRLSAGQWRSDMEDAHKAILNVKNTSTSIQIFDG 60
Db 1 MGQTLSEPVTAKEISAYCQNAAYRVGSSCMQWRINMEDSHTHLSLDPDPAFAFVYDG 60
Qy 61 HGGKLVAKFCAKHLHOVLKSEAYAGDLKASILEYSLRDEMKMGASGKELQSLLETS 120
Db 61 HGGATVAQYAGKHLHYLVLRPEY-NDNTEQALQQGFLDIDYVM----- 103
Qy 121 SOLDKLGNNGSSNAREDDSDSYAVLTESDNLATKKHKYSDFQGIYGSTAVVALI 180
Db 104 -----LRNKTCGDQ-----MAGSTAVVVLV 123
Qy 181 RGNKLFVANAGDSRCIMSRGEGAVNLSDHKPNLEHERKRIESAGGVHGGRVNGSLNT 240
Db 124 KDNKLYCANAGDSRAIACVNGQLEVLSDHKPNNEAESKRITIOGGGWVEFNRVNGNLALS 183
Qy 241 RAIGDMFEKGRPLDPDKQVTCPPDVVEVDLPGDFEIVLACDGIWDMVSSQAVVDFVK 300
Db 184 RALGCDYVFK-HENKPEQDQIVTAFDPVETRKIMDDWEFIVLACDGIWDMVSSQAVVDFVK 242
Qy 301 SRLPTTKTTLSSICEEILDYCLSPTRTQQE-GCDNMSSIIIV 339
Db 243 TRIGMGMPPEICEELMNHCLAPDCQMGLGSDNMTVVLV 282
RESULT 6
Q9W0Q0 ID Q9W0Q0 PRELIMINARY; PRT; 352 AA.
AC Q9W0Q0
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-OCT-2001 (TReMBLrel. 18, Last annotation update)
DE CG12169 PROTEIN.
GN CG12169
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_Taxid=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY.
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
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RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
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RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Smith H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
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RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,
RA Balow R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
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RA Foslter C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Hostin D., Houston K.A., Howland T.J., Hernandez J.R., Houck J.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
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RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
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RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
RA "The genome sequence of Drosophila melanogaster."
RT Science 287:2185-2195(2000).
DR EMBL: AE003468; AAF47393.1; -.
DR HSSP: P35813; 1A60.
DR FlyBase: FBgn0035143; CG12169.
DR InterPro: IPR001922; PP2C.
DR InterPro: IPR001932; PP2C_domain.
DR Pfam: PF00481; PP2C; 1.
DR SMART: SM00332; PP2C; 1.
DR SMART: SM00333; PP2C-SIG; 1.
DR PROSITE: PS01032; PP2C; 1.
SQ SEQUENCE 352 AA; 38529 MW; D0D1A7CD7D6F53EC CRC64;

Query Match 30.1%; Score 552.5; DB 5; Length 352;
Best Local Similarity 37.2%; Pred. No. 1.6e-36;
Matches 127; Conservative 47; Mismatches 108; Indels 59; Gaps 4;

QY 1 MGILCSPKTKTSEDDENAEALRYGLSAMQGWDRSDMEADHAKLLNVKNTSTISFGIFDG 60
DB 1 MGQTLSEPTTKDTACCANASTRVSSCMQGWVRVDMEDAHTHILSLPDPQAAFFAVYDG 60

QY 61 HGKLVAKFCAKHLHOVLKSEAYAGDKLASLEYSFLRMD-EMMKGASGNKELQSLSEET 119
DB 61 HGGASVAKYAGKHLHLFTKREPYRDNSTIEVALKKAFLDFDREMLQNG-----SLDEQ 113

QY 120 SSQDLKLGNGSSNNAREDESQYAVVLTESNDNLATKKHKYSDFGPIYGVSTAVVAL 179
DB 120 TA-----GCTAIVVL 123

QY 180 IRGNKLVANAGDSRCIMSRGAEVNLSTIDKPNLEHRRKTESAGGFVHGRVNGSLNL 239
DB 124 IRRRLRYCANAGDSRAIACISGWHIALSVDPNDPAKESKRMASGSGWFEFNRVNGNAL 183

QY 240 TRAIGDMFKGRPDLPPDKQVVTCCPDVVVVDLGPGEFIVLACDGIWDMSSQAVDFV 299
DB 184 SRALGDFIYKLLKLTPEQIVTAYPDVEVLDTEDLEFVLLACDGIWDMNSFEVCQFV 243

QY 300 KSLPLTKTLSSICEILDYCLSPTRQ-OECGDNWSIIIV 339
DB 244 HKRIQDMPELICEELMNSCLSPDGHGTGNVGGDNNTIVL 284
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RESULT 7
Q9VBF9 PRELIMINARY; PRT; 367 AA.
AC Q9VBF9;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-OCT-2001 (TReMBLrel. 18, Last annotation update)
DE CG6036 PROTEIN.
GN CG6036.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Ananides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Pfeiffer B.D.,
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RA Balow R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
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RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Swirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
RA "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
DR EMBL: AE003756; AAF56583.1; -.
DR HSSP: P35813; 1A60.
DR FlyBase: FBgn0039421; CG6036.
DR InterPro: IPR000222; PP2C.
DR InterPro: IPR001932; PP2C_domain.
DR Pfam: PF00481; PP2C; 1.
DR SMART: SM00332; PP2C; 1.
DR SMART: SM00331; PP2C-SIG; 1.
DR PROSITE: PS01032; PP2C; 1.
SQ SEQUENCE 367 AA; 41214 MW; 14380A505621A173 CRC64;

Query Match 29.9%; Score 549; DB 5; Length 367;
Best Local Similarity 35.0%; Pred. No. 3.3e-36;
Matches 126; Conservative 61; Mismatches 103; Indels 70; Gaps 7;

QY 1 MGILCSPKTKTSEDDENAEALRYGLSAMQGWDRSDMEADHAKLLNV-DKNTSTISFGIFD 59
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Db 1 MGFLKPEKTEKQAGHGNGLRVCSSMOGRLEMEDESHSAACRLKDPFATWSYFAVFD 60
QY 60 GHGKLVAKFCAKHLHQEVLSKSEAYAKGLKASLEYSFLRMDMMKMGASGKELQSLBET 119
Db 61 GHAGSISLHCAEHLMSLILESEFSKHKYEAGIREGFLOJDEDMR----- 106
QY 120 SSOLDKLGNGSSNAREDDSDSYAVLTESNDSNLATKKHKYSDFQGPYIGSTAVVAL 179
Db 107 -----KL-----YHDOQG--GSTAICVF 122
QY 180 IRGNKLFVANAGDSRCIMSRGAEAVNLSIDHKPNLEHERKRIETESAGGFVHGVRNGSLNL 239
Db 123 VSPDKIYLVNCGDSRAVSRNGAAVLTIDHKPFSPKQERIONAGGSVMKIRINGTLAV 182
QY 240 TRAIGDMEFKGRDPLDPKQVVTCCPDVVEVDLGGDEFEIVLACDGIWDMVSSQAVDFV 299
Db 183 SRAFGDYDFKNGSKSPVQVSPEDTIIVCNRSRSEHDEFIVVACDGIWDMVMTSSEVCEFI 242
QY 300 KSLRPTTKTLLSSICEILDYCLSPTRQOEGCDNMSIIV-----OPK--QSGVAASSTD 353
Db 243 RSLRLTYDLPIMVNSVLDICLHKGR-----DNMTLLLLLPAGPKVDMDAVRAERSLD 297
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RESULT 8
Q9GVP5 ID Q9GVP5 PRELIMINARY; PRT; 280 AA.
AC Q9GVP5;
DT 01-MAR-2001 (TRENBLrel. 16, Created)
DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)
DE PHOSPHATASE 2C (FRAGMENT).
OS Sterkiella histriomuscorum.
OC Eukaryota; Alveolata; Ciliophora; hypotrichs; Stichotrichida;
OX Oxytrichidae; Sterkiella.
NCBI_TaxID=94289;
RN [1]
SEQUENCE FROM N.A.
RA Villalobo E., Moch C., Perasso R., Baroin-Tourancheau A.;
RT "Searching for excystment-regulated genes in Sterkiella
histriomuscorum (Ciliophora, Oxytrichidae): a mRNA differential
display analysis of gene expression in excysting cells.";
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF309503; AAG47769.1; -.
DR HSSP; P35813; 1A60.
DR InterPro; IPR000222; PP2C.
DR SMART; PF00481; PP2C; 1.
DR PFam; PF00481; PP2C; 1.
DR SMART; SM00332; PP2C; 1.
DR PROSITE; PS01032; PP2C; 1.
FT NON_TER 280
SQ SEQUENCE 280 AA; 31289 MW; 07252EE8D154CA82 CRC64;
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Query Match 29.7%; Score 545; DB 5; Length 280;
Best Local Similarity 41.3%; Pred. No. 4.8e-36;
Matches 124; Conservative 45; Mismatches 87; Indels 44; Gaps 7;
QY 1 MGILYSPKTDKTSDEENALRYGLSAMQGRDSDNEADHAKILNVKNTSTISFGIFDG 60
Db 1 MGDYLVDPKNHSESGDKHRTAFGATTWQGRKQTQEDAH--IARLDICDGNLSLFAVFDG 58
QY 61 HGKLVAKCAKHLHQEVLSKSEAYAKGLKASLEYSFLRMDMMKMGASGKELQSLBETS 120
Db 59 HGGDQVAKYAEKTMVQELLKLSYKDKYKKSLEEVFLKIDELM-----LQHIQ-- 108
QY 121 SOLDKLGNGSSNAREDDSDSYAVLTESNDSNLATKKHKYSDFQGPYIGSTAVVALI 180
Db 109 -----NG--SSGRSREDDYS-----ADPNLSES-----GCTSNVILI 139
QY 181 RGNKLFVANAGDSR-----CIMSRRGEAVNLSIDHKPNLEHERKRIETESAGGFVHGVRNGSL 237
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Db 140 TKDKIYCANAGDSRAVNCVFGSGPETFVELSHDHKPNETEKORIVNADGFVQMGRTNGVI 199
QY 238 NLTRAIGDMEFKGRDPLDPKQVVTCCPDVVEVDLGGDEFEIVLACDGIWDMVSSQAVVD 297
Db 200 SLSRALGDFDYKKKADFPPEKQATTAFPDVSEHDLTENCOFIVQACDGIWDCILTSPEAVD 259
RESULT 9
Q9VAK1 ID Q9VAK1 PRELIMINARY; PRT; 368 AA.
AC Q9VAK1;
DT 01-MAY-2000 (T-EMBLrel. 13, Created)
DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)
DT 01-OCT-2001 (TRENBLrel. 18, Last annotation update)
DE CG1906 PROTEIN.
GN CG1906.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Ananatiades P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazef R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abrial J.F., Agbayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,
RA Balow R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brockstein P., Brothier P.,
RA Burtis K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foslcr C., Gabrielian A.E., Gaig N.S., Gelbart W.M., Glasser K.,
RA Glodex A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinart K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Swirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-I., Wassarman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-E., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
DR EMBL; AC003770; AAF56905.1; -.
DR HSSP; P35813; 1A60.
DR FlyBase; FBgn0039672; CG1906.
DR InterPro; IPR000222; PP2C.
DR InterPro; IPR001932; PP2C_domain.
DR PFam; PF00481; PP2C; 1.
DR SMART; SM00332; PP2C; 1.
DR SMART; SM00331; PP2C_SIG; 1.
DR PROSITE; PS01032; PP2C; 1.
DR PROSITE; PS01032; PP2C; 1.
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QY 120 SSQDKLGNSSNAREDESYSVLTESDNSLTKKHYSDFQPIYGSFAVAL 179
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QY	288
Db	247

Qy 288 DVMSQAAYVDFVKSRSLPTTKTSSLCSEILDYCLSPTRQQEGCDNMSIIV---QPKQ 343
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Db 247 DVMSNEELCEEFVKSRLEVSDDLNVNCWVVDTLHKGSR----DNMSVVLVCFSNAPKV 301

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QY 344 SGVAASSTD 353
Db 302 SEAVKRDSE 311

RESULT 12
Q9HAY8 PRELIMINARY; PRT; 387 AA.
AC Q9HAY8;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE SER/THR PROTEIN PHOSPHATASE TYPE 2C BETA 2 ISOFORM (PROTEIN
DE PHOSPHATASE 1B1 43 KDA ISOFORM) (PROTEIN PHOSPHATASE 2C-LIKE
DE PROTEIN).
GN PPM1B1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A.
RX PubMed=10945995;
RA Cheng A., Kaldis P., Solomon M.J.;
RT "Dephosphorylation of Human Cyclin-dependent Kinases by Protein
RT Phosphatase Type 2Calpha and beta2 Isoforms.";
RL J. Biol. Chem. 275:34744-34749(2000).
RN [2]
SEQUENCE FROM N.A.
RA Seroussi E., Shani N., Hayut A., Falier S., Ben-Meir D., Divinski I.,
RA Smorodinsky N.I., Lavi S.;
RT "Protein phosphatase 1B. Cloning and characterization of two major
RT transcripts generated by alternative use of 3' exons.";
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
SEQUENCE FROM N.A.
RC TISSUE=ADRENAL GLAND;
RA Peng Y., Gu Y., Li Y., Fu S., Gu J., Zhang L., Jiang C., Yu Y.,
RA Han Z., Wang Y., Chen Z., Fu G.;
RT "A novel gene expressed in human adrenal gland.";
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
RN [4]
SEQUENCE FROM N.A.
RC TISSUE=ADRENAL GLAND;
RA Wu T., Gu J., Ren S., Jin W., Fu S., Huang Q., Dong H., Yu Y., Fu G.,
RA Wang Y., Chen Z., Han Z.;
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF294792; AAC02232.1;
DR EMBL; AJ271835; CAC27993.1;
DR EMBL; AF136972; AAC49433.1;
DR HSSP; P35813; IAG0.
DR InterPro; IPR000222; PP2C.
DR InterPro; IPR001932; PP2C_domain.
DR Pfam; PF00481; PP2C; 1.
DR SMART; SM00332; PP2Cc; 1.
DR SMART; SM00331; PP2C_SIG; 1.
DR PROSITE; PS01032; PP2C; 1.
SQ SEQUENCE 387 AA; 42771 MW; 56A644A4E5E2B12B CRC64;

Query Match 29.3%; Score 538; DB 4; Length 387;
Best Local Similarity 34.6%; Pred. No. 2.8e-35;
Matches 128; Conservative 57; Mismatches 109; Indels 76; Gaps 7;

QY 1 MGIYLCSPKTKTSEDDENAEURLYGLSAMQWRDSMEDAHKAILNVDRNTST-SIFGIFD 59
Db 1 MGAFLDKPKTERKHAHAGNGLRYGLSSMQGWRVEMDAHTAVGIPHGLEDWSEFFAVYD 60

QY 60 GHGKGLVAKFCAKHLHQLKSEAY-AKGDLSKASLEYS-----FLRMDMMKGA 107
Db 61 GHAGSRVANCYSTHLLHETITNEDFRAAGKSGSALESVENKNGIRTGFLKIDEYHRNF 120

QY 1 MGIYLCSPKTKTSEDDENAEURLYGLSAMQWRDSMEDAHKAILNVDRNTST-SIFGIFD 59
Db 1 MGAFLDKPKTERKHAHAGNGLRYGLSSMQGWRVEMDAHTAVGIPHGLEDWSEFFAVYD 60

QY 60 GHGKGLVAKFCAKHLHQLKSEAY-AKGDLSKASLEYS-----FLRMDMMKGA 107
Db 61 GHAGSRVANCYSTHLLHETITNEDFRAAGKSGSALESVENKNGIRTGFLKIDEYHRNF 120

Query Match 29.1%; Score 534; DB 11; Length 465;
Best Local Similarity 34.3%; Pred. No. 7.6e-35;
Matches 125; Conservative 54; Mismatches 109; Indels 76; Gaps 6;

QY 1 MGIYLCSPKTKTSEDDENAEURLYGLSAMQWRDSMEDAHKAILNVDRNTST-SIFGIFD 59
Db 1 MGAFLDKPKTERKHAHAGNGLRYGLSSMQGWRVEMDAHTAVGIPHGLEDWSEFFAVYD 60

QY 60 GHGKGLVAKFCAKHLHQLKSEAY-AKGDLSKASLEYS-----FLRMDMMKGA 107
Db 61 GHAGSRVANCYSTHLLHETITNEDFRAAGKSGFALEPSVENKVTGRTGFLKIDEYMRNF 120

QY 108 SGWKELOSLEETSSQLDKLGNSSNAREDDSDYSYAVLTESNDSNLATKKHKYSDFQ 167
Db 121 S-----DLRNGMDRS----- 130

QY 168 GPTYGSTAVVALIRGNKLFVANAGDSRCITMSRRGEAVNLSIDHKPNLEHERKRIESAGF 227
Db 131 -----GSTAVGVMLSPHIYFINGDSRAVLRCNGQVCFSTQDHKPCNPMEKRIQAGGS 186

QY 228 VHGGVRVNSLNLTRATGDMFEKGRDLPDPKQVVTCCPDVVEVDLPGDGFIVLACDGIW 287
Db 302 SDEAVKRDSE 311

RESULT 13
Q99ND8 PRELIMINARY; PRT; 465 AA.
AC Q99ND8;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE PROTEIN PHOSPHATASE 1B2 53 KDA ISOFORM.
GN PPM1B2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
SEQUENCE FROM N.A.
RA Seroussi E., Shani N., Hayut A., Falier S., Ben-Meir D., Divinski I.,
RA Smorodinsky N.I., Lavi S.;
RT "Protein phosphatase 1B. Cloning and characterization of two major
RT transcripts generated by alternative use of 3' exons.";
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ271834; CAC28066.1;
DR HSSP; P35813; IAG0.
DR InterPro; IPR000222; PP2C.
DR InterPro; IPR001932; PP2C_domain.
DR Pfam; PF00481; PP2C; 1.
DR SMART; SM00332; PP2Cc; 1.
DR SMART; SM00331; PP2C_SIG; 1.
DR PROSITE; PS01032; PP2C; 1.
SQ SEQUENCE 465 AA; 51010 MW; A94DB476C48FC136 CRC64;

Query Match 29.1%; Score 534; DB 11; Length 465;
Best Local Similarity 34.3%; Pred. No. 7.6e-35;
Matches 125; Conservative 54; Mismatches 109; Indels 76; Gaps 6;

QY 1 MGIYLCSPKTKTSEDDENAEURLYGLSAMQWRDSMEDAHKAILNVDRNTST-SIFGIFD 59
Db 1 MGAFLDKPKTERKHAHAGNGLRYGLSSMQGWRVEMDAHTAVGIPHGLEDWSEFFAVYD 60

QY 60 GHGKGLVAKFCAKHLHQLKSEAY-AKGDLSKASLEYS-----FLRMDMMKGA 107
Db 61 GHAGSRVANCYSTHLLHETITNEDFRAAGKSGFALEPSVENKVTGRTGFLKIDEYMRNF 120

QY 108 SGWKELOSLEETSSQLDKLGNSSNAREDDSDYSYAVLTESNDSNLATKKHKYSDFQ 167
Db 121 S-----DLRNGMDRS----- 130

QY 168 GPTYGSTAVVALIRGNKLFVANAGDSRCITMSRRGEAVNLSIDHKPNLEHERKRIESAGF 227
Db 131 -----GSTAVGVMLSPHIYFINGDSRAVLRCNGQVCFSTQDHKPCNPMEKRIQAGGS 186

QY 228 VHGGVRVNSLNLTRATGDMFEKGRDLPDPKQVVTCCPDVVEVDLPGDGFIVLACDGIW 287
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Db 187 VMIQVNGSLAVSRALGDDYDKCVDGKPTQELVSPPEVYELIRAEDEFVYLACDGIW 246
QY 288 DVMSQAVVDVFKSRPTTKTSLSSCEILDYCLSTPTTQOQCGDNMSIIIV----QPKQ 343
Db 247 DVMSNEELCFVNSRLEVSDDLNVNCWVVDVCLHKGR-----DNMSIVLCFANAPKV 301
QY 344 SGVA 347
Db 302 SDEA 305
RESULT 14
Q9EQE2 PRELIMINARY; PRT; 323 AA.
AC Q9EQE2;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE PROTEIN PHOSPHATASE 2C ALPHA 1B.
GN P2C1B.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Chermiack A.D., Nicoloro S.M.C., Buxton J.M., Bose A., Emoto M.,
Waters S.B., Czech M.P.;
RT "Potentiation of Insulin Receptor Signaling by Protein Phosphatase
2C.";
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF259673; AAG44662.1; -;
DR HSSP; P35813; 1A6Q.
DR InterPro; IPR000222; PP2C.
DR InterPro; IPR001932; PP2C_domain.
DR Pfam; PF00481; PP2C; 1.
DR SMART; SM00332; PP2C; 1.
DR SMART; SM00331; PP2C_SIG; 1.
DR PROSITE; PS01032; PP2C; 1.
SQ SEQUENCE 323 AA; 35888 MW; 83B6E793AE816B9 CRC64;
Query Match 28.3%; Score 519; DB 11; Length 323;
Best Local Similarity 33.9%; Pred. No. 7.3e-34;
Matches 124; Conservative 59; Mismatches 111; Indels 72; Gaps 8;
QY 1 MGIYLCSPKTDKTSSEDDENAEALRYGLSAMQGRDSMEDAHKAILNVDKNTST-SIFGIFD 59
Db 1 MGAFLDKPRMEKHNAQGGNGRLYGLSSMOGRVEMEDAHTAVIGLPSGLETWSFFAYVD 60
QY 60 GHGKLVAKFCAKHLHGOEVLKSE-----AYAKGLKASLEYSFLRMDMMKASGWKE 112
Db 61 GHAGSQVAKYCCCHLLDHTNNQDFRGSAGAPSVENKNGIRTGLEIDEHMR----- 113
QY 113 LQSLKETSSQLDKLNGNSSNAREDDSDSYAVULTESNDSNLATKKHKYSDFQGIYV 172
Db 114 -----VMSE-----KKH-----GADRS 126
QY 173 STAVVALIRGNKLFVANAGDSRCIMSRGGEAVNLSIDHKPNLEHKKRTESAGGFVHGR 232
Db 127 STAVGLISPHQHYFFINCDSRGLLCRNKRVHFTQDHRKPSNPLEKRIQONAGGSVMIOR 186
QY 233 VNGSLNLTIRAGDMFKGRPDLPDKQVVTCCPDVVEVDLG-PGDEFIVLACDGIWVMS 291
Db 187 VNGSLAVSRALGDFDKCVHKGPTQLVSPPEVHDIERSEDDQFIILACDGIWVNG 246
QY 292 SOAVVDVFKSRPTTKTSLSSCEILDYCLSTPTTQOQCGDNMSIIIV----QPKQSGVA 347
Db 247 NEELCDFVRSRLEVTDDLEKVCNEVVDTCLYKGR-----DNMSVILICFSPAPKVSAB 301
QY 348 ASSSTD 353
Db 302 SDEA 305

Db 302 VKKEAE 307
RESULT 15
Q9EQE3 PRELIMINARY; PRT; 326 AA.
AC Q9EQE3;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE PROTEIN PHOSPHATASE 2C ALPHA 3.
GN P2CA3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Chermiack A.D., Nicoloro S.M.C., Buxton J.M., Bose A., Emoto M.,
Waters S.B., Czech M.P.;
RT "Potentiation of Insulin Receptor Signaling by Protein Phosphatase
2C.";
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF259672; AAG44661.1; -;
DR HSSP; P35813; 1A6Q.
DR InterPro; IPR000222; PP2C.
DR InterPro; IPR001932; PP2C_domain.
DR Pfam; PF00481; PP2C; 1.
DR SMART; SM00332; PP2C; 1.
DR SMART; SM00331; PP2C_SIG; 1.
DR PROSITE; PS01032; PP2C; 1.
SQ SEQUENCE 326 AA; 36110 MW; 19AA1994931A823B CRC64;
Query Match 28.3%; Score 519; DB 11; Length 326;
Best Local Similarity 33.9%; Pred. No. 7.4e-34;
Matches 124; Conservative 59; Mismatches 111; Indels 72; Gaps 8;
QY 1 MGIYLCSPKTDKTSSEDDENAEALRYGLSAMQGRDSMEDAHKAILNVDKNTST-SIFGIFD 59
Db 1 MGAFLDKPRMEKHNAQGGNGRLYGLSSMOGRVEMEDAHTAVIGLPSGLETWSFFAYVD 60
QY 60 GHGKLVAKFCAKHLHGOEVLKSE-----AYAKGLKASLEYSFLRMDMMKASGWKE 112
Db 61 GHAGSQVAKYCCCHLLDHTNNQDFRGSAGAPSVENKNGIRTGLEIDEHMR----- 113
QY 113 LQSLKETSSQLDKLNGNSSNAREDDSDSYAVULTESNDSNLATKKHKYSDFQGIYV 172
Db 114 -----VMSE-----KKH-----GADRS 126
QY 173 STAVVALIRGNKLFVANAGDSRCIMSRGGEAVNLSIDHKPNLEHKKRTESAGGFVHGR 232
Db 127 STAVGLISPHQHYFFINCDSRGLLCRNKRVHFTQDHRKPSNPLEKRIQONAGGSVMIOR 186
QY 233 VNGSLNLTIRAGDMFKGRPDLPDKQVVTCCPDVVEVDLG-PGDEFIVLACDGIWVMS 291
Db 187 VNGSLAVSRALGDFDKCVHKGPTQLVSPPEVHDIERSEDDQFIILACDGIWVNG 246
QY 292 SOAVVDVFKSRPTTKTSLSSCEILDYCLSTPTTQOQCGDNMSIIIV----QPKQSGVA 347
Db 247 NEELCDFVRSRLEVTDDLEKVCNEVVDTCLYKGR-----DNMSVILICFSPAPKVSAB 301
QY 348 ASSSTD 353
Db 302 VKKEAE 307

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OM protein - protein search, using sw model

Run on: June 19, 2002, 08:44:06 ; Search time 13.42 Seconds
(without alignments)
1018.480 Million cell updates/sec

Title: US-09-828-302-14
Perfect score: 1836
Sequence: 1 MGILCSPKTKTSTEDENA.....MSIIIVQPKQSGVAASSTD 353

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	643	35.0	546	1 P2CG_HUMAN	O15355 homo sapien
2	641.5	34.9	542	1 P2CG_MOUSE	O61074 mus musculus
3	641	34.9	543	1 P2CG_BOVIN	P09126 bos taurus
4	635	34.6	370	1 P2C2_SCHPO	Q09172 schizosacch
5	616.5	33.6	300	1 P2C2_PARTE	Q49444 paramacium
6	608.5	33.1	414	1 P2C3_SCHPO	Q09173 schizosacch
7	606	33.0	356	1 P2C2_CAEEL	P49596 caenorhabdi
8	555.5	30.3	491	1 P2C1_CAEEL	P49595 caenorhabdi
9	554.5	30.2	464	1 P2C2_YEAST	P39866 saccharomyc
10	539	29.4	390	1 P2CB_MOUSE	P36993 mus musculus
11	538	29.3	479	1 P2CB_HUMAN	O75688 homo sapien
12	537	29.2	387	1 P2CB_BOVIN	O62830 bos taurus
13	537	29.2	468	1 P2C3_YEAST	P34221 saccharomyc
14	534	29.1	390	1 P2CB_RAT	P35815 rattus norv
15	522	28.4	382	1 P2CA_RAT	P20650 rattus norv
16	521	28.4	382	1 P2CA_BOVIN	O62829 bos taurus
17	520	28.3	382	1 P2CA_RABIT	P35814 oryctolagus
18	519	28.3	382	1 P2CA_MOUSE	P49443 mus musculus
19	517	28.2	382	1 P2CA_HUMAN	P35813 homo sapien
20	398.5	21.7	393	1 YB5_YEAST	P38089 saccharomyc
21	357.5	19.5	423	1 P2C1_ARATH	O04719 arabidopsis
22	354	19.3	434	1 P2C1_ARATH	P49597 arabidopsis
23	350.5	19.1	388	1 P2C3_ARATH	P49599 arabidopsis
24	343.5	18.7	347	1 P2C1_SCHPO	P40371 schizosacch
25	341.5	18.6	281	1 P2C1_YEAST	P35182 saccharomyc
26	334	18.2	399	1 P2C4_ARATH	P49598 arabidopsis
27	326	17.8	406	1 P2C2_LEICH	P36982 leishmania
28	298.5	16.3	454	1 P2CH_HUMAN	P49593 homo sapien
29	253	13.8	2493	1 CVAA_USTMA	P49606 ustilago ma
30	247	13.5	1839	1 CVAA_SACKL	P23466 saccharomyc
31	242.5	13.2	449	1 FEM2_CAEEL	P49594 caenorhabdi
32	242.5	13.2	2026	1 CFAA_YEAST	P08678 saccharomyc
33	239	13.0	605	1 P2CD_HUMAN	O15297 homo sapien

34	235	12.8	598	1 P2CD_MOUSE	O9qz67 mus musculus
35	223	12.1	530	1 PDP2_RAT	O88484 rattus norv
36	222.5	12.1	538	1 PDP1_RAT	O88483 rattus norv
37	218.5	11.9	538	1 PDP1_BOVIN	P35816 bos taurus
38	218	11.9	2300	1 CVAA_NEOCR	Q01631 neurospora
39	217.5	11.8	538	1 PDP1_HUMAN	O9p011 homo sapien
40	205.5	11.2	2145	1 CVAA_PODAN	Q01513 podospira a
41	203.5	11.1	529	1 PDP2_HUMAN	O9p219 homo sapien
42	190	10.3	581	1 KAPP_ARATH	P46014 arabidopsis
43	172	9.4	1692	1 CVAA_SCHPO	P14605 schizosacch
44	158	8.6	383	1 P2C4_SCHPO	O14156 schizosacch
45	156.5	8.5	504	1 TAB1_HUMAN	Q15750 homo sapien

ALIGNMENTS

RESULT 1	
P2CG_HUMAN	
ID	P2CG_HUMAN
AC	O15355;
DT	15-JUL-1998 (Rel. 36, Created)
DT	15-JUL-1998 (Rel. 36, Last sequence update)
DT	16-OCT-2001 (Rel. 40, Last annotation update)
DE	Protein phosphatase 2C gamma isoform (EC 3.1.3.16) (PP2C-gamma)
DE	(Protein phosphatase magnesium-dependent 1 gamma) (Protein phosphatase 1C).
DE	1C).
GN	PPMIG OR PPMIC.
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX	NCBI_TaxID=9606;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE=Skeletal muscle;
RX	MEDLINE=97420453; PubMed=9276438;
RA	Travis S.M., Welsh M.J.;
RT	"PP2C gamma: a human protein phosphatase with a unique acidic
RT	domain.";
RL	FEBs Lett. 412:415-419(1997).
RN	[2]
RP	SEQUENCE FROM N.A.
RC	TISSUE=Placenta;
RA	Strausberg R.;
RL	Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
CC	!- CATALYTIC ACTIVITY: A PHOSPHOPROTEIN + H(2)O = A PROTEIN +
CC	ORTHOPHOSPHATE (THIS ENZYME IS SERINE/THREONINE SPECIFIC).
CC	!- COFACTOR: BINDS 2 MAGNESIUM OR MANGANESE IONS (BY SIMILARITY).
CC	!- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC	!- TISSUE SPECIFICITY: WIDELY EXPRESSED. MOST ABUNDANT IN TESTIS,
CC	SKELETAL MUSCLE, AND HEART.
CC	!- SIMILARITY: BELONGS TO THE PP2C FAMILY.
CC	-----
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CC	or send an email to license@isb-sib.ch).
CC	-----
DR	EMBL; Y13936; CAA74245.1; -
DR	EMBL; BC000057; AAH00057.1; -
DR	HSSP; P35813; 1A6Q.
DR	MIM; 605119; -
DR	InterPro; IPR000222; PP2C.
DR	InterPro; IPR001932; PP2C_domain.
DR	Pfam; PF00481; PP2C; 2.
DR	SMART; SM00331; PP2C_SIG; 1.
DR	SMART; SM00332; PP2C; 1.
DR	PROSITE; PS01032; PP2C; 1.
KW	Hydrolase; Magnesium; Manganese; Multigene family.
FT	METAL 40 40 MANGANESE 1 (BY SIMILARITY).

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FT METAL 41 41 MANGANESE 1 (BY SIMILARITY).
FT METAL 60 60 MANGANESE 1 AND 2 (BY SIMILARITY).
FT METAL 441 441 MANGANESE 2 (BY SIMILARITY).
FT METAL 496 496 MANGANESE 2 (BY SIMILARITY).
FT DOMAIN 258 326 ASP/GLU-RICH ACIDIC.
FT DOMAIN 266 272 POLY-GLU.
FT DOMAIN 306 311 POLY-LYS.
FT DOMAIN 539 544 POLY-LYS.
SQ SEQUENCE 546 AA; 59271 MW; 084C16F8252330D9 CRC64;

Query Match 35.0%; Score 643; DB 1; Length 546;
Best Local Similarity 32.7%; Pred. No. 2,4e-42;
Matches 165; Conservative 60; Mismatches 112; Indels 168; Gaps 9;

Qy 1 MGIYLSPKTKDTSDEDDENA---ELRYGLSAMOGWRSDMEDAHKAILNVKNTSIFGI 57
Db 1 MGAYLSQPNVTKSGDGVGAPRLPLPYGFSAMOGWRVSMEDAHNCIPELD--SETAMFSV 58
Qy 58 FDHGGKLVAKFCAKHLHQELKSEAYAKGDLKASLEYSLRMDMMKASGKWL--- 113
Db 59 YDGHGGEVALYCAKYLPLDIKDKAYKEGKQKALEDAFLDAIDAKLTTEEVIKELAQIA 118
Qy 114 ----- 113
Db 119 GRPTEDEDEKEVADEDDVDNEEAALLHEEATMTIEELLTRYQNCCHKGPHPSKGGGTG 178
Qy 114 -----QSLKETSSOLD-----KLGNGSSSNAR----- 136
Db 179 EEPGSQLNGEAGPEDSRTPTSQENGPTAKAYTGFSNSERGTEAGQVGEPGPTGAG 238
Qy 137 -----EDDESYSYAVLTESDSDNLSATKKHYDFQ----- 167
Db 239 PSCSSASDKLPRVAKSKFFEDSEDEAEEDSECEDEEDGYSSBEAEENEDEDT 298
Qy 168 -----GPIYGSTAVVALIRGNKLFVANAGDSRCIMSRGE 202
Db 299 EEAEDDEEEEMVPMGCKEESDGGTAVVALIRGNKLFVANAGDSRCVSEAGK 358
Qy 203 AVNLSIDHKPNLEHRRKIESAGGFV-HGGRVNGSLNLTFRAGDMFEKGRPLDPDKQV 261
Db 359 ALDMSYDHPKEDEVELARIKAGGKVTMDGRVNGSLNLTFRAGDMFEKGRPLDPDKQV 418
Qy 262 TCCPDVVEVDLPGDFIVLACGIWVMSQAVDFVKSRLP-----TTKTLSSLCEE 315
Db 419 SALPDIVLITDHDHFWJACDGIWVMSQAVDFVKSRLP-----TTKTLSSLCEE 478
Qy 316 ILDYCLSP-TTROEGCDNNMIIIV 339
Db 479 LLDQCLAPDTSGBTGCDNNMTCIII 503

RESULT 2
P2CG_MOUSE STANDARD; PRT; 542 AA.
ID P2CG_MOUSE
AC Q61074;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Protein phosphatase 2C gamma isoform (EC 3.1.3.16) (P2CG-gamma)
DE (Protein phosphatase magnesium-dependent 1 gamma) (Protein phosphatase
DE 1C) (Fibroblast growth factor inducible protein 13) (FIN13).
GN PPM1G OR PPMIC OR FIN13.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A., FUNCTION, AND SUBCELLULAR LOCATION.
RX MEDLINE=97415625; PubMed=9271424;
RA Guthridge M.A., Bellosta P., Belloni N., Basilico C.;
RT "FIN13, a novel growth factor-inducible serine-threonine phosphatase
RT which can inhibit cell cycle progression.";
```

```
RL Mol. Cell. Biol. 17:5485-5498(1997).
RN [2]
RP SEQUENCE OF 123-420 FROM N.A.
RX MEDLINE=96226358; PubMed=8649829;
RA Guthridge M.A., Seldin M., Basilico C.;
RT "Induction of expression of growth-related genes by FGF-4 in mouse
RT fibroblasts.";
RL Oncogene 12:1267-1278(1996).
CC -1- FUNCTION: MAY BE INVOLVED IN REGULATION OF CELL CYCLE.
CC -1- CATALYTIC ACTIVITY: A PHOSPHOPROTEIN + H(2)O = A PROTEIN +
CC ORTHOPHOSPHATE (THIS ENZYME IS SERINE/THREONINE SPECIFIC).
CC -1- COFACTOR: BINDS 2 MAGNESIUM OR MANGANESE IONS (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN TESTIS. LOW LEVEL OF
CC EXPRESSION IN KIDNEY. ALSO EXPRESSED IN A NUMBER OF TISSUES
CC UNDERGOING PROLIFERATION INCLUDING EMBRYO, UTERUS AT PREGNANCY,
CC PLACENTA, AND OVARIES.
CC -1- INDUCTION: BY FIBROBLAST GROWTH FACTOR 4 AND SERUM.
CC -1- SIMILARITY: BELONGS TO THE P2C FAMILY.
CC -----
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CC -----
CC EMBL; U42383; AAC26322.1; --
CC HSP; P35813; IAG0.
CC MGD; MGI:106065; Pmlg.
CC InterPro; IPR000222; P2C.
CC InterPro; IPR001932; P2C_domain.
CC Pfam; PF00481; P2C; 2.
CC SMART; SM00331; P2C_SIG; 1.
CC SMART; SM00332; P2C_C; 1.
CC PROSITE; PS01032; P2C; 1.
CC Hydrolase; Magnesium; Manganese; Multigene family; Nuclear protein;
KW Metal-binding; Cell cycle.
FT METAL 40 40 MANGANESE 1 (BY SIMILARITY).
FT METAL 41 41 MANGANESE 1 (BY SIMILARITY).
FT METAL 60 60 MANGANESE 1 AND 2 (BY SIMILARITY).
FT METAL 438 438 MANGANESE 2 (BY SIMILARITY).
FT METAL 493 493 MANGANESE 2 (BY SIMILARITY).
FT DOMAIN 258 319 ASP/GLU-RICH (ACIDIC).
FT CONFLICT 123 126 EDED -> NSAR (IN REF. 2).
SQ SEQUENCE 542 AA; 58728 MW; 1DC7E7A66E71453 CRC64;

Query Match 34.9%; Score 641.5; DB 1; Length 542;
Best Local Similarity 31.9%; Pred. No. 3.1e-42;
Matches 161; Conservative 63; Mismatches 111; Indels 169; Gaps 9;

Qy 1 MGIYLSPKTKDTSDEDDENA---ELRYGLSAMOGWRSDMEDAHKAILNVKNTSIFGI 57
Db 1 MGAYLSQPNVTKSGDGVGAPRLPLPYGFSAMOGWRVSMEDAHNCIPELD--NETAMFSV 58
Qy 58 FDHGGKLVAKFCAKHLHQELKSEAYAKGDLKASLEYSLRMDMM----- 104
Db 59 YDGHGGEVALYCAKYLPLDIKDKAYKEGKQKALEDAFLDAIDAKLTTEEVIKELAQIA 118
Qy 105 ----- 104
Db 119 GRPTEDEDDKVADEDDVDNEEAALLHEEATMTIEELLTRYQNCQKVPHTKSGIGTG 178
Qy 105 -----KGSAGWK----- 111
Db 179 DEFGPQNGEAGPEPSRETPTSQENGPTAKGHTGFSNSEHGTEAGQISEPGTATGAG 238
Qy 112 -----ELQSLFETSSQLDKLGNNGNSSNA-REDESDY 143
Db 239 PSCSSASDKLPRVAKSKFFEDSEDESEDEEDSECEDEEDGYSSBEAEENEDEDT 298
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Qy 144 SYAVLTESNDNSLTKKHKYSDFQPIYGSTAVVALIRGNKLFVANAGDSRCIMSRGEA 203
 Db 299 EEA--EDDDDEEMVPGMEGKEEPCSGSTTAVVALIRGNKLIIVANAGDSRCVSEAGKA 356
 Qy 204 VNLSDHKPNLEHERKRIESAGGFV-HGGRVNGSLNLTTRAIGDMFEKGRDPLPPDKQVVT 262
 Db 357 LDMSYDHKPEDEVELARIKNAGGKVTMDGRVNGSLNLTTRAIGDHFYKRNKLNLPPEQOMIS 416
 Qy 263 CCPDVVEVDLGPDEFIVLACDGIWDMVSSQAVVDVFKSRLP-----TTKTLSSICEEI 316
 Db 417 ALPDIKVLTLTDDHFMFIACDGIWNVMSQEVVDFIQSKISQDENGELRLSSIVEEL 476
 Qy 317 LDVCLSP-TTROQEGCDNMIIIV 339
 Db 477 LDQCLAPDTSQDGTGCDNMTCIII 500

RESULT 3
 P2CG_BOVIN STANDARD; PRT; 543 AA.
 AC P79126;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Protein phosphatase 2C gamma isoform (EC 3.1.3.16) (PP2C-gamma)
 DE (Protein phosphatase magnesium-dependent 1 gamma) (Protein phosphatase
 DE 1B) (Magnesium-dependent calcium inhibitable phosphatase) (MCPP).
 GN PM1G OR PM1C.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Huang C.Y., Qin K.;
 RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: A PHOSPHOPROTEIN + H(2)O = A PROTEIN +
 CC ORTHOPHOSPHATE ('THIS ENZYME IS SERINE/THREONINE SPECIFIC').
 CC COFACTOR: BINDS 2 MAGNESIUM OR MANGANESE IONS (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
 CC -1- SIMILARITY: BELONGS TO THE PP2C FAMILY.
 CC -----
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 CC -----
 DR EMBL; U01159; AAB39357.1; -;
 DR HSPB; P35813; IAGQ.
 DR InterPro; IPR000222; PP2C.
 DR InterPro; IPR001932; PP2C_domain.
 DR Pfam; PF00481; PP2C; 2.
 DR SMART; SM00331; PP2C_SIG; 1.
 DR SMART; SM00332; PP2CC; 1.
 DR PROSITE; PS01032; PP2C; 1.
 KW Hydrolyase; Magnesium; Manganese; Multigene family.
 FT METAL 40 40 MANGANESE 1 (BY SIMILARITY).
 FT METAL 41 41 MANGANESE 1 (BY SIMILARITY).
 FT METAL 60 60 MANGANESE 1 AND 2 (BY SIMILARITY).
 FT METAL 439 439 MANGANESE 1 (BY SIMILARITY).
 FT METAL 494 494 MANGANESE 2 (BY SIMILARITY).
 FT DOMAIN 258 324 ASP/GLU-RICH ACIDIC.
 FT DOMAIN 266 272 POLY-GLU.
 FT DOMAIN 306 309 POLY-GLU.
 SQ SEQUENCE 543 AA; 58708 MW; DD1898195E234A94 CRC64;

Query Match 34.9%; Score 641; DB 1; Length 543;
 Best Local Similarity 32.0%; Pred. No. 3.4e-42;

Matches 164; Conservative 64; Mismatches 118; Indels 166; Gaps 10;
 Qy 1 MGIYLCSPKTDKTSDEENAE---LAYGLSAMQGRWDSMEDAHKAILNVDKNTSTISIRGI 57
 Db 1 MGAYLSOPNTVKSGDGVGASRLPLPYGFSAMQGRWVSMEDAHNCTIQLD--SETAMFSV 58
 Qy 58 FDHGGLKLVAKFCAKHLHQEVLSKSEAYAKGDLKASLEYSLRMDENMMKGASGKELQSL- 116
 Db 59 YDHGGEEVALYCAKYLIPDIKDKQAYKEGKLQKALEDAFLDAKLITTEEVIKELAQIA 118
 Qy 117 -----BETSSQLDKL-----GNG 129
 Db 119 GRPTEDEKEKVADEDDVDNEEAALLHEATMTIEELLTRYGQNCHKGAPHSKSGAGTG 178
 Qy 130 NS-----SSNAR----- 136
 Db 179 EEPGSQLNGEAGEPDPSPRETSAEVNGPTAKAHTGLSSNSECGTEAGOGGEGPTGTGAG 238
 Qy 137 -----EDDESYSYAVLTESNDNSLTKKHKYSDFQ----- 167
 Db 239 PSCSSASDKLPRVDKSKFFEDSEDEAEDEEEDSECESEEDGYSEEAENEDEDDT 298
 Qy 168 -----GPIYGVSTAVVALIRGNKLFVANAGDSRCIMSRGEAV 204
 Db 299 EEAEDDEEEMVPGMEGKEEPCSGSTTAVVALIRGNKLIIVANAGDSRCVSEAGKA 358
 Qy 205 NLSIDHKPNLEHERKRIESAGGFV-HGGRVNGSLNLTTRAIGDMFEKGRDPLPPDKQVVT 263
 Db 359 DMSYDHKPEDEVELARIKNAGGKVTMDGRVNGSLNLTTRAIGDHFYKRNKLNLPPEQOMISA 418
 Qy 264 CPDVVEVDLGPDEFIVLACDGIWDMVSSQAVVDVFKSRLP-----TTKTLSSICEEI 317
 Db 419 LPDIKVLTLTDDHFMFIACDGIWNVMSQEVVDFIQSKISQDENGELRLSSIVEYLL 478
 Qy 318 DYCLSP-TTROQEGCDNMIIIVOPKOSGVAA 348
 Db 479 DQCLAPDTSQDGTGCDNMTCIIICFKPRNTAA 510

RESULT 4
 P2C2_SCHPO STANDARD; PRT; 370 AA.
 ID P2C2_SCHPO
 AC Q09172;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Protein phosphatase 2C homolog 2 (EC 3.1.3.16) (PP2C-2).
 GN PTC2 OR SPCC123.11.
 OS Schizosaccharomyces pombe (fission yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;
 OX NCBI_TaxID=4896;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-972;
 RA MEDLINE=95163582; PubMed=7859738;
 RA Shiozaki K., Russell P.;
 RT "Counteractive roles of protein phosphatase 2C (PP2C) and a MAP
 RT kinase kinase homolog in the osmoregulation of fission yeast.";
 RL EMBO J. 14:492-502(1995).
 RL [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-972;
 RA wedler H., Wambutt R., Lyne M., Rajandream M.A., Barrell B.G.;
 RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: HAS AN IMPORTANT ROLE IN OSMOTIC STABILITY AND CELL
 CC SHAPE CONTROL. IT MAY NEGATIVELY REGULATE THE OSMOSENSING SIGNAL
 CC TRANSMITTED THROUGH WIS1 MAP KINASE.
 CC -1- CATALYTIC ACTIVITY: A PHOSPHOPROTEIN + H(2)O = A PROTEIN +
 CC ORTHOPHOSPHATE (THIS ENZYME IS SERINE/THREONINE SPECIFIC).
 CC -1- COFACTOR: BINDS 2 MAGNESIUM OR MANGANESE IONS (BY SIMILARITY).
 CC -1- SUBUNIT: MONOMER.

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CC CC -!- SIMILARITY: BELONGS TO THE PP2C FAMILY.
CC CC -----
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CC CC -----
CC CC EMBL; L34881; AAA67320.1; -.
CC CC EMBL; AL031579; CAA20880.1; -.
CC CC HSP; P35813; IA6Q.
CC CC InterPro; IPR000222; PP2C.
CC CC InterPro; IPR001932; PP2C_domain.
CC CC Pfam; PF00481; PP2C; 1.
CC CC SMART; SM00331; PP2C_SIG; 1.
CC CC SMART; SM00332; PP2C; 1.
CC CC PROSITE; PS01032; PP2C; 1.
CC CC Hydrolase; Magnesium; Manganese; Multigene family.
CC CC METAL 37 37 MANGANESE 1 (BY SIMILARITY).
CC CC METAL 38 38 MANGANESE 1 (BY SIMILARITY).
CC CC METAL 63 63 MANGANESE 1 AND 2 (BY SIMILARITY).
CC CC METAL 233 233 MANGANESE 2 (BY SIMILARITY).
CC CC METAL 282 282 MANGANESE 2 (BY SIMILARITY).
CC CC SEQUENCE 370 AA; 40878 MW; DBDB826F440AC50 CRC64;
CC CC -----
CC CC Query Match 34.6%; Score 635; DB 1; Length 370;
CC CC Best Local Similarity 41.6%; Pred. No. 5.9e-42;
CC CC Matches 144; Conservative 48; Mismatches 90; Indels 64; Gaps 8;
CC CC
CC CC 1 MGIVLCSPKDTSEDDENAEALRYGLSAMQWRDSMEDAHKAILN-VDKNTS---TSIFG 56
CC CC 1 MGQTLSEPLVDKHSSSGDRWLHFGVSHMQWRISMEDAHKALLNFTDSNSSNPPTSFFG 60
CC CC
CC CC 57 IFDGHGKLVAKCAKHLHGVLEKSE-AYAKGLKASLEYSFLRMDMMKGASGKELQIS 115
CC CC 61 VFDGHGDRVAKYCRQHL-PPDIISQSPFWKNGYDALKSGFLAAD----- 105
CC CC 116 LEETSSQLDKLNGNSSNAREDDSDSYAVLTSNDSNLATKKHKYSDFQGIYGSTA 175
CC CC 106 -----NALMQDR-----DMQEDPSGCTA 123
CC CC 176 VVALIRGNK-LFVANAGDSRCIMSRGEAVNLSDHKPNLEHERKRIESAGGFVHGGRVN 234
CC CC 124 TTALIVHQVIYCANAGDSRTVLGRGTAPLSFDHKPNNDVEKARITAAAGGFIDFGRVN 183
CC CC 235 GSLNLTRAIGDMFEKGRPDLPDPKQVVTCCPDVVEVDLGGDEFFIVLACDGIWDMSSQA 294
CC CC 184 GSLALSRAIGDFEYKDSLPPEKQIVTAPDVVVIHNDPDEFLILACDGIWDCKSSQ 243
CC CC 295 VDFVKSRLPTTKYLSLCEIILDYCLSPTRQ-QEGCDNMIIIV 339
CC CC 244 VVEFVRGIVAROSLEVICENLMDRCIASNSCSGIGCDNMTCIV 289
CC CC
CC CC RESULT 5
CC CC P2C_PARTE STANDARD; PRT; 300 AA.
CC CC ID P2C_PARTE
CC CC AC P49444;
CC CC DT 01-FEB-1996 (Rel. 33, Created)
CC CC DT 01-FEB-1996 (Rel. 33, Last sequence update)
CC CC DT 01-NOV-1997 (Rel. 35, Last annotation update)
CC CC DE Protein phosphatase 2C (EC 3.1.3.16) (PP2C).
CC CC OS Paramecium tetraurelia.
CC CC Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Peniculida;
CC CC Paramecium.
CC CC NCBI_TaxID=5888;
CC CC [1]
CC CC SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
CC CC STRAIN=51S;
CC CC MEDLINE=95105156; PubMed=7806499;
```

```
RA Klumpp S., Hanke C., Donella-Deana A., Beyer A., Kellner R.,
RA Pinna L.A., Schultz J.E.;
RA "A membrane-bound protein phosphatase type 2C from Paramecium
RA tetraurelia. Purification, Characterization, and cloning.";
RA J. Biol. Chem. 269:32774-32780(1994).
RA CC -!- FUNCTION: ENZYME WITH A BROAD SPECIFICITY.
RA CC -!- CATALYTIC ACTIVITY: A PHOSPHOPROTEIN + H(2)O -> A PROTEIN +
RA CC ORTHOPHOSPHATE (THIS ENZYME IS SERINE/THREONINE SPECIFIC).
RA CC -!- COFACTOR: BINDS 2 MAGNESIUM OR MANGANESE IONS (BY SIMILARITY).
RA CC -!- SUBCELLULAR LOCATION: Membrane-bound.
RA CC -!- SIMILARITY: BELONGS TO THE PP2C FAMILY.
RA CC -----
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RA CC -----
RA CC EMBL; Z36985; CAA85448.1; -.
RA CC HSP; P35813; IA6Q.
RA CC InterPro; IPR000222; PP2C.
RA CC InterPro; IPR001932; PP2C_domain.
RA CC Pfam; PF00481; PP2C; 1.
RA CC SMART; SM00331; PP2C_SIG; 1.
RA CC SMART; SM00332; PP2C; 1.
RA CC PROSITE; PS01032; PP2C; 1.
RA CC Hydrolase; Magnesium; Manganese; Membrane.
RA CC METAL 37 37 MANGANESE 1 (BY SIMILARITY).
RA CC METAL 38 38 MANGANESE 1 (BY SIMILARITY).
RA CC METAL 57 57 MANGANESE 1 AND 2 (BY SIMILARITY).
RA CC METAL 237 237 MANGANESE 2 (BY SIMILARITY).
RA CC METAL 289 289 MANGANESE 2 (BY SIMILARITY).
RA CC SEQUENCE 300 AA; 33739 MW; BC0318B4FF772AEC CRC64;
RA CC
RA CC Query Match 33.6%; Score 616.5; DB 1; Length 300;
RA CC Best Local Similarity 38.5%; Pred. No. 1.2e-40;
RA CC Matches 132; Conservative 61; Mismatches 99; Indels 51; Gaps 4;
RA CC
RA CC 1 MGIVLCSPKDTSEDDENAEALRYGLSAMQWRDSMEDAHKAILNVDKNTSIFGFDG 60
RA CC 1 MGYPLOSPEKDKTTTGGQKSVIFAASEMQWRNTMEDAH-IHRHDIIDQVSVFVGFDG 58
RA CC 61 HGKLVAKFCAKHLHGVLEKSEAYAKGLKASLEYSFLRMDMMKGASGKELQLEETS 120
RA CC 59 HGGREVAQFVEKHFVDELLKKNKFKQKPEALKETFLKMDLELLTPEGKELNQYKAT- 117
RA CC 121 SOLDKLNGNSSNAREDDSDSYAVLTSNDSNLATKKHKYSDFQGIYGSTAVVALI 180
RA CC 118 -----DTDESIA-----CCTANVALI 133
RA CC 181 RGNKLFVANAGDSRCIMSRGEAVNLSDHKPNLEHERKRIESAGGFVHGGRVNSLNT 240
RA CC 134 YKNTLYVANAGDSKSLCRNNTNHDMSVDHKPDNPEKSRIERAGGFVSDGRVNGNLNS 193
RA CC 241 RAICDMFEKGRPDLPDPKQVVTCCPDVVEVDLGGDEFFIVLACDGIWDMSSQAVDFVK 300
RA CC 194 RALGDLKRYKRNKRLSRNEQIIFALPDVKKTELPDQKFIIDMGCDGVFTLNHQLKQVN 253
RA CC 301 SRL----PTTKTSLSSCEIILDYCLSPTRRQEGCDNMIIIV 339
RA CC 254 STIGQAQVTEELKKAEDLLDQLAPDTSQGTGCDNMIIIV 296
RA CC
RA CC RESULT 6
RA CC P2C3_SCHPO STANDARD; PRT; 414 AA.
RA CC ID P2C3_SCHPO
RA CC AC Q09173;
RA CC DT 01-NOV-1995 (Rel. 32, Created)
RA CC DT 01-NOV-1995 (Rel. 32, Last sequence update)
```

```

01-NOV-1997 (Rel. 35, Last annotation update)
PTC3 OR SPAC2G11.07C.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OX Schizosaccharomycetes.
OX NCBI_TaxID=4896;
[1]
RN SEQUENCE FROM N.A.
RP STRAIN=972;
RC MEDLINE=95163582; PubMed=7859738;
RX Shiozaki K., Russell P.;
RT "Counteractive roles of protein phosphatase 2C (PP2C) and a MAP
RT kinase homolog in the osmoregulation of fission yeast.";
RL EMBO J. 14:492-502(1995).
[2]
RN SEQUENCE FROM N.A.
RP STRAIN=972;
RC Badcock K., Churcher C.M., Barrell B.G., Rajandream M.A., Walsh S.V.;
RA Submitted (OCT-1995) to the EMBL/GenBank/DBJ databases.
RL -!- FUNCTION: HAS AN IMPORTANT ROLE IN OSMOTIC STABILITY AND CELL
CC SHAPE CONTROL. IT MAY NEGATIVELY REGULATE THE OSMOSENSING SIGNAL
CC TRANSMITTED THROUGH WIS1 MAP KINASE.
CC -!- CATALYTIC ACTIVITY: A PHOSPHOPROTEIN + H(2)O = A PROTEIN +
CC ORTHOPHOSPHATE (THIS ENZYME IS SERINE/THREONINE SPECIFIC).
CC -!- COFACTOR: BINDS 2 MAGNESIUM OR MANGANESE IONS (BY SIMILARITY).
CC -!- SUBUNIT: MONOMER.
CC -!- SIMILARITY: BELONGS TO THE PP2C FAMILY.
-----
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CC or send an email to license@isb-sib.ch).
-----
CC EMBL; L34882; AAA67321.1; -.
CC EMBL; Z54354; CAA91172.1; -.
CC HSP; P35813; IAGQ.
CC InterPro; IPR000222; PP2C.
CC InterPro; IPR001932; PP2C_domain.
CC Pfam; PF00481; PP2C; 1.
CC SMART; SM00331; PP2C_SIG; 1.
CC SMART; SM00332; PP2CC; 1.
CC PROSITE; PS01032; PP2C; 1.
CC Hydrolase; Magnesium; Manganese; Multigene family.
CC METAL 37 37 MANGANESE 1 (BY SIMILARITY).
CC METAL 38 38 MANGANESE 1 (BY SIMILARITY).
CC METAL 62 62 MANGANESE 1 AND 2 (BY SIMILARITY).
CC METAL 230 230 MANGANESE 2 (BY SIMILARITY).
CC METAL 279 279 MANGANESE 2 (BY SIMILARITY).
CC CONFLICT 196 196 K -> T (IN REF. 1).
CC SEQUENCE 414 AA; 44856 MW; EFF3A416625A2B11 CRC64;

Query Match 33.1%; Score 608.5; DB 1; Length 414;
Best Local Similarity 40.2%; Pred. No. 7.6e-40;
Matches 138; Conservative 48; Mismatches 96; Indels 61; Gaps 5;

QY 1 MGIVLCPKTDKTSDEENAEALRYGLSAMOGWRDSEDAHKALINVDKNT---STSIQI 57
DB 1 MGQTLSEPVTEKHSVNGSNEFVLYGLSSMOGWRISMEDAHSAILLSNECSAVKDPVDFAV 60

QY 58 PDGHHGKLVAKFKAKHLHQEVLEKSEAYAKGDLKASLEYFLRDEMKGASGWLQSL 117
DB 61 YDGHGGDKVAKWCGSNLPQILEKNPDQFKGDFVNAKSSFLNADKAI----- 107

QY 118 ETSSQDKLGNNGSSNAREDDSDSYAVLITSDNSLTKKHKYSDFQGIYGTAV 177
DB 108 -----LDDQ-----FHTDPGCTATV 124

178 ALIRGNKLFVANAGDSRCIMSRGEAVNLSIDHKPNLEHERKRIESAGGFVHGVRVNGSL 237
125 VLRVGNKLYCANAGDSFTVLGSGIAKPLSADHKPSNEAKARICARGFVDFGRVNGNL 184
238 NLTRAIGDMFEKGRDLPDPKQVVTCCPDVVVDLPGDFEFIVLACDGIWDVSSQAVVD 297
185 ALSRAIGDFEFK-NSNLEPEKQIVTALPDVVVHEITDDDFEVVVLACDGIWDCKTSQOVIE 243
298 FVKSRLPTTKTSLSCIEILDYCL-SPTTRQOQEGCDNMSIIV 339
244 FVRGIVACTSLEKIAENLMDNCIASDTETTGLCDDNMTVCIV 286

RESULT 7
P2C2 CAEEL
ID P2C2 CAEEL STANDARD; PRT; 356 AA.
AC P49596;
DT 01-FEB-1996 (Rel. 33, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Probable protein phosphatase 2C T23F11.1 (EC 3.1.3.16) (PP2C).
GN T23F11.1.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
[1]
RN SEQUENCE FROM N.A.
RP STRAIN-BRISTOL N2;
RC Swinburne J.;
RL Submitted (OCT-1994) to the EMBL/GenBank/DBJ databases.
[2]
RN REVISIONS.
RP Durbin R.;
RA Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
CC -!- CATALYTIC ACTIVITY: A PHOSPHOPROTEIN + H(2)O = A PROTEIN +
CC ORTHOPHOSPHATE (THIS ENZYME IS SERINE/THREONINE SPECIFIC).
CC -!- COFACTOR: BINDS 2 MAGNESIUM OR MANGANESE IONS (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE PP2C FAMILY.
-----
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CC or send an email to license@isb-sib.ch).
-----
CC EMBL; Z46343; CAA86456.2; -.
CC HSP; P35813; IAGQ.
CC Wormpep; T23F11.1; CE24009.
CC InterPro; IPR000222; PP2C.
CC InterPro; IPR001932; PP2C_domain.
CC Pfam; PF00481; PP2C; 1.
CC SMART; SM00331; PP2C_SIG; 1.
CC SMART; SM00332; PP2CC; 1.
CC PROSITE; PS01032; PP2C; 1.
CC Hypothetical protein; Hydrolase; Magnesium; Manganese.
CC METAL 37 37 MANGANESE 1 (BY SIMILARITY).
CC METAL 38 38 MANGANESE 1 (BY SIMILARITY).
CC METAL 59 59 MANGANESE 1 AND 2 (BY SIMILARITY).
CC METAL 228 228 MANGANESE 2 (BY SIMILARITY).
CC METAL 277 277 MANGANESE 2 (BY SIMILARITY).
CC SEQUENCE 356 AA; 39064 MW; EDCB0841CFB026B5 CRC64;

Query Match 33.0%; Score 606; DB 1; Length 356;
Best Local Similarity 37.0%; Pred. No. 9.8e-40;
Matches 131; Conservative 58; Mismatches 103; Indels 62; Gaps 4;

QY 1 MGIVLCPKTDKTSDEENAEALRYGLSAMOGWRDSEDAHKALINVDKNTSIFIGF 60
DB 1 MGQTLSEPVTEKHSASCANENYLVGSSCMQGRVDMEDAHTHLLSLPDDPKCAFFAVYDG 60
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 CC -----

DR EMBL; U18839; AAB64644.1; -;
 DR EMBL; U72498; AAB17392.1; -;
 DR HSSP; P35813; 1A60.
 DR SGD; S0000891; PTC2.
 DR InterPro; IPR000222; PP2C.
 DR InterPro; IPR001932; PP2C_domain.
 DR Pfam; PF00481; PP2C; 1.
 DR SMART; SM00331; PP2C_SIG; 1.
 DR SMART; SM00332; PP2C; 1.
 DR PROSITE; PS01032; PP2C; 1.
 KW Hydrolase; Magnesium; Manganese; Multigene family.
 FT METAL 37 37 MANGANESE 1 (BY SIMILARITY).
 FT METAL 38 38 MANGANESE 1 (BY SIMILARITY).
 FT METAL 62 62 MANGANESE 1 AND 2 (BY SIMILARITY).
 FT METAL 234 234 MANGANESE 2 (BY SIMILARITY).
 FT METAL 283 283 MANGANESE 2 (BY SIMILARITY).
 SQ SEQUENCE 464 AA; 50388 MW; 61D82D2CA4ED3FED CRC64;

Query Match 30.2%; Score 554.5; DB 1; Length 464;

Best Local Similarity 36.8%; Pred. No. 1.3e-35;

Matches 133; Conservative 50; Mismatches 113; Indels 65; Gaps 7;

QY 1 MGILSPKTDKTSDEDAEALRYGLSAMQWRDSMEDAHKAILNV-----DKNTSTSTFG 56
 Db 1 MGQILSNPYVDKESHGADSLAFGLCAMQGRMSWEDSHILEPNVLTKSKDK-HIAPYG 59
 QY 57 IFDGHGKLVAKCAKHLHQEVKLSAYAKDLKASLEYSFLRMDMMKSGAWKELQSL 116
 Db 60 IFDGHGAKVYCGNKGKIVKILQEQKSEHGNLPRALIDTFTNDVKLLQDPVAKKE----- 115
 QY 117 EETSSQLDKLGNSSNAREDESYSVAVLTESNLSLTKKHKYSDFQPIYGVSTAV 176
 Db 116 -----DHS-----GCTAT 123
 QY 177 VALI--RGNKLFVANAGDSRCIMSRGEAVNLSIDHKPNLEHKKRISAGFVHGGRVN 234
 Db 124 SILVSKSNQLVYGNAGDSRTLATDGNKALSVDHKPTLASEKSRIVAAADPGFVEMDRVN 183
 QY 235 GSNLTRAIGDMFEKGRPDLPDPKQVVTCCPDVWEVDLG-PGDEFIVLACDGIWDMSSQ 293
 Db 184 GNLSAIGAIDFEKSNPKLGPEEQIVTCVPDILEHSLDYDEDFVILLACDGIWDLTSQ 243
 QY 294 AVVDFVKSLPTTKTLSSICEILDYCLSPTRQOE-GCDNMSTIIVQPKSGVAASSST 352
 Db 244 DCVDLHLGLREGKTLNEISSRIIDVCCAPTTEGTGIGCDNMSTIIVVALLKEGEDVAQWS 303
 QY 353 D 353
 Db 304 D 304

RESULT 10

P2CB_MOUSE
 ID P2CB_MOUSE STANDARD; PRT; 390 AA.
 AC P36993;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DE 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Protein phosphatase 2c beta isoform (EC 3.1.3.16) (PP2C-beta) (IA)
 DE (Protein phosphatase 1B).
 GN PPM1B OR PPM1B OR PP2C2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;

RN
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94099616; PubMed=8274020;
 RA Tanaka T., Kobayashi T., Murakami T., Ohnishi M., Kato S.,
 RA Tanaka O., Kondo H., Yamamoto H., Takeuchi T., Tamura S.;
 RT "Molecular cloning of a novel isotype of Mg(2+)-dependent protein
 RT phosphatase beta (type 2C beta) enriched in brain and heart.";
 RL Arch. Biochem. Biophys. 307:342-349(1993).
 RN [2]
 RP SEQUENCE FROM N.A. (BETA-3; BETA-4 AND BETA-5).
 RC TISSUE=Testis;
 RX MEDLINE=95251388; PubMed=7733667;
 RA Kato S., Terasawa T., Kobayashi T., Ohnishi M., Sasahara Y.,
 RA Kusuda K., Yanagawa Y., Hiraga A., Matsui Y., Tamura S.;
 RT "Molecular cloning and expression of mouse Mg(2+)-dependent protein
 RT phosphatase beta-4 (type 2C beta-4).";
 RL Arch. Biochem. Biophys. 318:387-393(1995).
 RN [3]
 RP SEQUENCE FROM N.A. (BETA-3 AND BETA-4).
 RC TISSUE=Testis;
 RX MEDLINE=94313028; PubMed=8038726;
 RA Hou E.W., Kawai Y., Miyasaka H., Li S.S.;
 RT "Molecular cloning and expression of cDNAs encoding two isoforms of
 RT protein phosphatase 2C beta from mouse testis.";
 RL Biochem. Mol. Biol. Int. 32:773-780(1994).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/SV;
 RX MEDLINE=99398339; PubMed=10469137;
 RA Ohnishi M., Chida N., Kobayashi T., Wang H., Ikeda S., Hanada M.,
 RA Yanagawa Y., Katsura K., Hiraga A., Tamura S.;
 RT "Alternative promoters direct tissue-specific expression of the mouse
 RT protein phosphatase 2c beta gene.";
 RL Eur. J. Biochem. 263:736-745(1999).
 CC -!- FUNCTION: ENZYME WITH A BROAD SPECIFICITY.
 CC -!- CATALYTIC ACTIVITY: A PHOSPHOPROTEIN + H(2)O = A PROTEIN +
 CC ORTHOPHOSPHATE (THIS ENZYME IS SERINE/THREONINE SPECIFIC).
 CC -!- COFACTOR: BINDS 2 MAGNESIUM OR MANGANESE IONS (BY SIMILARITY).
 CC -!- SUBUNIT: MONOMER (BY SIMILARITY).
 CC -!- ALTERNATIVE PRODUCTS: 5 ISOFORMS; BETA-1 (SHOWN HERE), BETA-2,
 CC BETA-3, BETA-4 AND BETA-5; ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC THEY ONLY DIFFER IN THEIR C-TERMINUS.
 CC -!- TISSUE SPECIFICITY: BETA-1 IS EXPRESSED UBQUITOUSLY; BETA-2 IS
 CC EXPRESSED EXCLUSIVELY IN BRAIN AND HEART; BETA-4 IS EXPRESSED
 CC EXCLUSIVELY IN BRAIN AND INTESTINE; BETA-3 AND BETA-5 ARE
 CC EXPRESSED EXCLUSIVELY IN TESTIS AND INTESTINE.
 CC -!- SIMILARITY: BELONGS TO THE PP2C FAMILY.
 CC -----
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 CC -----
 DR EMBL; D17411; BAA04233.1; -;
 DR EMBL; D17412; BAA04234.1; -;
 DR EMBL; D45859; BAA08293.1; -;
 DR EMBL; D45860; BAA08294.1; -;
 DR EMBL; D45861; BAA08295.1; -;
 DR EMBL; U09218; AAB60442.1; -;
 DR EMBL; AB007798; BAA84471.1; -;
 DR EMBL; AB007794; BAA84471.1; JOINED.
 DR EMBL; AB007795; BAA84471.1; JOINED.
 DR EMBL; AB007796; BAA84471.1; JOINED.
 DR EMBL; AB007797; BAA84471.1; JOINED.
 DR PIR; S39780; S39780.
 DR HSSP; P35813; 1A60.
 DR MGD; MGI:101841; Pm1b.
 DR InterPro; IPR000222; PP2C.
 DR InterPro; IPR001932; PP2C_domain.
 DR Pfam; PF00481; PP2C; 1.

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DR SMART; SM00331; PP2C_SIG; 1.
DR SMART; SM00332; PP2C; 1.
DR PROSITE; PS01032; PP2C; 1.
KW Hydrolase; Magnesium; Manganese; Multigene family;
KW Alternative splicing.
FT METAL 37 MANGANESE 1 (BY SIMILARITY).
FT METAL 38 MANGANESE 1 (BY SIMILARITY).
FT METAL 60 MANGANESE 1 AND 2 (BY SIMILARITY).
FT METAL 243 MANGANESE 2 (BY SIMILARITY).
FT METAL 286 MANGANESE 2 (BY SIMILARITY).
FT VARSPLIC 379 GAGLDELSVAL -> VSLHLPKYLK (IN ISOFORM BETA-2).
FT VARSPLIC 390 GAGLDELSVAL -> FYQPSIAYSDNVFLL (IN ISOFORM BETA-3).
FT VARSPLIC 390 GAGLDELSVAL -> MADLSTICKPS (IN ISOFORM BETA-4).
FT VARSPLIC 388 VAL -> FYQPSIAYSDNVFLL (IN ISOFORM BETA-5).
FT VARSPLIC 390 AA; 42795 MW; 255C97B4276189FD CRC64;
SQ SEQUENCE 390 AA; 42795 MW; 255C97B4276189FD CRC64;

Query Match 29.4%; Score 539; DB 1; Length 390;
Best Local Similarity 33.5%; Pred. No. 1.7e-34;
Matches 124; Conservative 58; Mismatches 112; Indels 76; Gaps 6;

Qy 1 MGIYLCSPKTKTSEDENAEALRYGLSAMQGRDSDMEDAHKAILNVKNTST-SIFGIFD 59
Db 1 MGAFLDPKPKTEKHAAGNAGNGLRYGLSSMQGRVEMEDAHAVVGIPIHGLDWNSEFAVVD 60
Qy 60 GHGKLVAKCAKHLHOEVLKSEAYAKGP-----LKASLEYSLFLRDEMKGKA 107
Db 61 GHAGSRVANTCYSTHLLHITTFEDFRAADKSGSALEPVSVEKGTGRTGFLKIDYMRNF 120
Qy 108 SGWKELOSLEETSQDLKLGNGSSNAREDDSDSYAVLTESNDSNLATKKHKYSDFQ 167
Db 121 S-----DLRNGMDRS----- 130
Qy 168 GPIYGSTAVVALLINGKNLFVANAGDSRCIMSRGEAVNLSIDHKPNLEHERKRIESAGGF 227
Db 131 ----GSTAVGVMSPTHYMFINGDSRAVLICRNGQVCFSTQDHKPCNPVEKERIQNAGGS 186
Qy 228 VHGRVNGSLNLTARIGDMFEKGRPDLPPDKQVVTCCPDVVEVDLPGDGFIVLACDGIW 287
Db 187 VMIOVRVNGSLAVSRALGDYDKVCDKGTEQLVSPPEVEIYVRAEEDFEVVLACDGIW 246
Qy 288 DVMSQAVVDVFKSRUPTTKTLLSLCEEILDYCLSTPTTQEGCDNMSTIIIV----OPKQ 343
Db 247 DVMSNEELCEBFVKSRLEVSDDLNVNVCNVVVDTCCLKGSR-----DNMSVVLVCFNSAPKV 301
Qy 344 SGVAASSTSD 353
Db 302 SEEA VKRDE 311

RESULT 11
P2CB_HUMAN STANDARD; PRT; 479 AA.
AC 075688;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Protein phosphatase 2C beta isoform (EC 3.1.3.16) (PP2C-beta).
GN PMIB OR PP2CB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=98348020; PubMed=9684878;
RA Marely A.E., Kline A., Crabtree G., Sullivan J.E., Beri R.K.;
RT "The cloning expression and tissue distribution of human PP2Cbeta.";
```

```
RL FEBS Lett. 431:121-124(1998).
CC -I- FUNCTION: ENZYME WITH A BROAD SPECIFICITY.
CC -I- CATALYTIC ACTIVITY: A PHOSPHOPROTEIN + H(2)O = A PROTEIN + ORTHOPHOSPHATE (THIS ENZYME IS SERINE/THREONINE SPECIFIC).
CC -I- COFACTOR: BINDS 2 MAGNESIUM OR MANGANESE IONS (BY SIMILARITY).
CC -I- SUBUNIT: MONOMER (BY SIMILARITY).
CC -I- ALTERNATIVE PRODUCTS: A NUMBER OF ISOFORMS SUCH AS BETA-X (SHOWN HERE) ARE PRODUCED BY ALTERNATIVE SPLICING. THEY ONLY DIFFER IN THEIR C-TERMINUS.
CC -I- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN HEART AND SKELETAL MUSCLE.
CC -I- SIMILARITY: BELONGS TO THE PP2C FAMILY.
CC -----
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CC -----
DR EMBL; AJ005801; CAA06704.1; -.
DR HSP; P35813; IAGQ.
DR MIM; 603770; -.
DR InterPro; IPR000222; PP2C.
DR InterPro; IPR001932; PP2C_domain.
DR Pfam; PF00481; PP2C; 1.
DR SMART; SM00331; PP2C_SIG; 1.
DR SMART; SM00332; PP2C; 1.
DR PROSITE; PS01032; PP2C; 1.
KW Hydrolase; Magnesium; Manganese; Multigene family;
KW Alternative splicing.
FT METAL 37 37 MANGANESE 1 (BY SIMILARITY).
FT METAL 38 38 MANGANESE 1 (BY SIMILARITY).
FT METAL 60 60 MANGANESE 1 AND 2 (BY SIMILARITY).
FT METAL 243 243 MANGANESE 2 (BY SIMILARITY).
FT METAL 286 286 MANGANESE 2 (BY SIMILARITY).
SQ SEQUENCE 479 AA; 52642 MW; A3A5797AD263DFB CRC64;

Query Match 29.3%; Score 538; DB 1; Length 479;
Best Local Similarity 34.6%; Pred. No. 2.6e-34;
Matches 128; Conservative 57; Mismatches 109; Indels 76; Gaps 7;

Qy 1 MGIYLCSPKTKTSEDENAEALRYGLSAMQGRDSDMEDAHKAILNVKNTST-SIFGIFD 59
Db 1 MGAFLDPKPKTEKHAAGNAGNGLRYGLSSMQGRVEMEDAHAVVGIPIHGLDWNSEFAVVD 60
Qy 60 GHGKLVAKCAKHLHOEVLKSEAY-AKGD LKASLEYS-----FLRDEMKGKA 107
Db 61 GHAGSRVANTCYSTHLLHITTFEDFRAADKSGSALEPVSVEKGTGRTGFLKIDYMRNF 120
Qy 108 SGWKELOSLEETSQDLKLGNGSSNAREDDSDSYAVLTESNDSNLATKKHKYSDFQ 167
Db 121 S-----DLRNGMDRS----- 130
Qy 168 GPIYGSTAVVALLINGKNLFVANAGDSRCIMSRGEAVNLSIDHKPNLEHERKRIESAGGF 227
Db 131 ----GSTAVGVMSPTHYMFINGDSRAVLICRNGQVCFSTQDHKPCNPVEKERIQNAGGS 186
Qy 228 VHGRVNGSLNLTARIGDMFEKGRPDLPPDKQVVTCCPDVVEVDLPGDGFIVLACDGIW 287
Db 187 VMIOVRVNGSLAVSRALGDYDKVCDKGTEQLVSPPEVEIYVRAEEDFEVVLACDGIW 246
Qy 288 DVMSQAVVDVFKSRUPTTKTLLSLCEEILDYCLSTPTTQEGCDNMSTIIIV----OPKQ 343
Db 247 DVMSNEELCEBFVKSRLEVSDDLNVNVCNVVVDTCCLKGSR-----DNMSVVLVCFNSAPKV 301
Qy 344 SGVAASSTSD 353
Db 302 SEEA VKRDE 311

RESULT 12
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P2CB_BOVIN
ID P2CB_BOVIN STANDARD; PRT; 387 AA.
AC O62830;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE protein phosphatase 2C beta isoform (EC 3.1.3.16) (PP2C-beta).
GN PM1B.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Retina;
RX MEDLINE=98146173; PubMed=9486768;
RA Klump S., Selke D., Fischer D., Baumann A., Mueller F., Thanos S.;
RT "Protein phosphatase type-2C isozymes present in vertebrate retinas;
RT purification, characterization, and localization in photoreceptors.";
RL J. Neurosci. Res. 51:328-338(1998).
CC -!- FUNCTION: ENZYME WITH A BROAD SPECIFICITY.
CC -!- CATALYTIC ACTIVITY: A PHOSPHOPROTEIN + H(2)O = A PROTEIN +
CC ORTHOPHOSPHATE (THIS ENZYME IS SERINE/THREONINE SPECIFIC).
CC -!- COFACTOR: BINDS 2 MAGNESIUM OR MANGANESE IONS (BY SIMILARITY).
CC -!- SUBUNIT: MONOMER (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE PP2C FAMILY.
CC
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CC
CC EMBL; AJ005458; CAA06555.1; -.
CC HSP; P35813; IAG0.
CC InterPro: IPR000222; PP2C.
CC InterPro: IPR001932; PP2C_domain.
CC Pfam: PF00481; PP2C; 1.
CC SMART; SM00331; PP2C_SIG; 1.
CC SMART; SM00332; PP2C; 1.
CC PROSITE; PS01032; PP2C; 1.
CC Hydrolase; Magnesium; Manganese; Multigene family.
CC METAL 37 37 MANGANESE 1 (BY SIMILARITY).
CC METAL 38 38 MANGANESE 1 (BY SIMILARITY).
CC METAL 60 60 MANGANESE 1 AND 2 (BY SIMILARITY).
CC METAL 243 243 MANGANESE 2 (BY SIMILARITY).
CC METAL 286 286 MANGANESE 2 (BY SIMILARITY).
CC METAL 387 AA; 42834 MW; D70B95141250FFB1 CRC64;
SQ
Query Match 29.2%; Score 537; DB 1; Length 387;
Best Local Similarity 34.9%; Pred No. 2,4e-34;
Matches 129; Conservative 56; Mismatches 109; Indels 76; Gaps 7;
QY 1 MGYLSPKTDKTSDEDAEALRYGLSAQGWDRSDMAHRAILNVKNTST-SIFGIFD 59
DB 1 MGAFLDKPKTEKHNAHGAGNGLRYGLSSMQGWREMEADHTAVVGIPHGLEDWSPFAVYD 60
QY 60 GHGCKLVAKFCAKHLHOELVKSEAV-AKGDKASLEYS-----FLRMDMMKGA 107
DB 61 GHAGSRVANYCSTHLLHETINNEDEFRAGKSGSALEPSVENVKNGIRTFGLKIDEYMKRF 120
QY 108 SGWKLQSLKETTSOLDKLGNGNSSNAREDDSDSYAVLTESDNSLATKKHKYSDFQ 167
DB 121 S-----DLRNGMDRS----- 130
QY 168 GPIYGSTAVVALIRGNKLFVANAGDSRCIMSRGEAVNLSDHKPNLBERKRIESAGGF 227
DB 131 -----GSTAVGVMSIPKHIYFINGDSRAVLYRSGQVCFSTODHKPCNPREKERTQAGGS 186

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QY 228 VHGRVNGSLNLTRAIGDMEEFKGRPDLPDKQVITCCPDVVEVDLPGDEFTVLACDGIW 287
DB 187 VMTQRVNGSLAYSRALGDYDKVCKGTEQVLVSPEPEVYELRAEDEFILLACDGIW 246
QY 288 DVMSQAQVDFVKSRLPTTKTLSSCEELIDYCLSPTRFQQEGCDNMSTIIV-----QPKQ 343
DB 247 DVMSNELCEFEVKSRLVLESDDLNVNVMYVDTCLSHKGR-----DNMSIVLVCFSNAPKV 301
QY 344 SGVAASSTSD 353
DB 302 SDEAMRKDSE 311
RESULT 13
ID P2C3_YEAST STANDARD; PRT; 468 AA.
AC P34221; Q92330;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Protein phosphatase 2C homolog 3 (EC 3.1.3.16) (PP2C-3).
GN PTC3 OR YBL056W OR YBL0511 OR YBL0513.
OS Saccharomyces cerevisiae (Baker's Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C;
RX MEDLINE=94205266; PubMed=8154187;
RA Scherens B., el Bakkoury M., Vierendeels F., Dubois E., Messenguy F.;
RT "Sequencing and functional analysis of a 32,560 bp segment on the
RT left arm of yeast chromosome II. Identification of 26 open reading
RT frames, including the KIP1 and SEC17 genes.";
RL Yeast 9:1355-1371(1993).
RN [2]
RP SEQUENCE FROM N.A.
RA Maeda T., Wurliker-Murphy S.M., Saito H.;
RL Submitted (SEP-1996) to the EMBL/GenBank/DBAJ databases.
CC -!- CATALYTIC ACTIVITY: A PHOSPHOPROTEIN + H(2)O = A PROTEIN +
CC -!- ORTHOPHOSPHATE (THIS ENZYME IS SERINE/THREONINE SPECIFIC).
CC -!- COFACTOR: BINDS 2 MAGNESIUM OR MANGANESE IONS (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE PP2C FAMILY.
CC
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CC
CC EMBL; Z23261; CAA80791.1; -.
CC EMBL; Z35817; CAA84876.1; -.
CC EMBL; U72346; AAB17351.1; -.
CC PIR; S39832; S39832.
CC PIR; S37333; S37333.
CC HSP; P35813; IAG0.
CC SGD; S0000152; PTC3.
CC InterPro: IPR000222; PP2C.
CC InterPro: IPR001932; PP2C_domain.
CC Pfam: PF00481; PP2C; 1.
CC SMART; SM00331; PP2C_SIG; 1.
CC SMART; SM00332; PP2C; 1.
CC PROSITE; PS01032; PP2C; 1.
CC Hydrolase; Magnesium; Manganese; Multigene family.
CC METAL 37 37 MANGANESE 1 (BY SIMILARITY).
CC METAL 38 38 MANGANESE 1 (BY SIMILARITY).
CC METAL 62 62 MANGANESE 1 AND 2 (BY SIMILARITY).
CC METAL 234 234 MANGANESE 2 (BY SIMILARITY).
CC METAL 284 284 MANGANESE 2 (BY SIMILARITY).
CC CONFLICT 369 369 D -> G (IN REF. 2).
SQ SEQUENCE 468 AA; 51390 MW; DC5C1805382DC0D CRC64;

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Query Match      29.2%; Score 537; DB 1; Length 468;
Best Local Similarity 38.8%; Pred. No. 3e-34;
Matches 135; Conservative 38; Mismatches 109; Indels 66; Gaps 9;

QY 1 MGIVLCSPKTKTSEDDNAELRYGLSAMQGRWDSMEDAH---KAILNVKNTSTSIIFI 57
DB 1 MGQILSNPIIDKEHSGTDCITLAFGLCAMQGRWMSDEAHIVPEPNLLAESDEHIAFYGI 60

QY 58 FDHGGKLVAKFAKHLHQLKSEAYAKGDLKASLEYSFLRMD-EMKMGASGWKELQSL 116
DB 61 FDHGGSSVAEFCGSKMISILKQESFKSGMLEQCLIDFLATDVELLKD----- 110

QY 117 EETSSQLDKLGNSSNAREDESYSYAVLTESNDSNLATKKHYSDFQPIYGSTAV 176
DB 111 -----EKL-----KDHSS-----GCRAT 123

QY 177 VALIRGNK--LFVANAGDSRCIMSRGEAVNLSDHKPNLEHERKRIESAGGFVHGGRVN 234
DB 124 VILVSQKLKLLICANSQDSRTVLSTGNSKAMSFDBKPTLLSEKSRIVAADGFVEMDRVN 183

QY 235 GSNLNTRAIGDMFEKGRPDLPDPKQVVTCCPDVVEVDLG-PGDEFIVLACDINWMSQ 293
DB 184 GNLSLRAIGDFEFKNTKLGPEHQVVTCPDILCHNLNYDEDEIVILACDINWCLTSQ 243

QY 294 AVVDNRKSLRPT-TKTLSSLCEILDYCLSPTRQOE-GCDNMSIIV 339
DB 244 ECVDLVHYGISQGNMTLSDISSRIVDVCCSPTTEGSGICDNNMSIIV 291

RESULT 14
P2CB_RAT      STANDARD;      PRT;      390 AA.
AC P35815; Q64046;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE Protein phosphatase 2c beta isoform (EC 3.1.3.16) (PP2C-beta) (IA)
DE (Protein phosphatase 1B).
GN PPM1B OR PPM1B OR PP2C2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
SEQUENCE FROM N.A. (ISOFORM BETA-1).
RC TISSUE=Liver;
RX MEDLINE=92201367; PubMed=1312947;
RA Wenk J., Trompeter H.-I., Pettrich K.-G., Cohen P.T.W., Campbell D.G.,
RA Mieskes G.;
RT "Molecular cloning and primary structure of a protein phosphatase 2C
RT isoform.";
RL FEBS Lett. 297:135-138(1992).
RN [2]
SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=95169115; PubMed=7532404;
RA Schafer K., Braun T.;
RT "Monoclonal anti-FLAG antibodies react with a new isoform of rat Mg2+
RT dependent protein phosphatase beta.";
RL Biochem. Biophys. Res. Commun. 207:708-714(1995).
CC -1- FUNCTION: ENZYME WITH A BROAD SPECIFICITY.
CC -1- CATALYTIC ACTIVITY: A PHOSPHOPROTEIN + H(2)O = A PROTEIN +
CC ORTHOPHOSPHATE (THIS ENZYME IS SERINE/THREONINE SPECIFIC).
CC -1- COFACTOR: BINDS 2 MAGNESIUM OR MANGANESE IONS (BY SIMILARITY).
CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
CC -1- ALTERNATIVE PRODUCTS: A NUMBER OF ISOFORMS SUCH AS BETA-1 (SHOWN
CC HERE) AND BETA-MPP ARE PRODUCED BY ALTERNATIVE SPLICING. THEY ONLY
CC DIFFER IN THEIR C-TERMINUS.
CC -1- SIMILARITY: BELONGS TO THE PP2C FAMILY.
-----
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-----
CC EMBL; S90449; AAB21898.1; -.
CC EMBL; S74572; AAB33430.1; -.
CC PIR; S20392; S20392.
CC HSP; P35813; 1A60.
CC InterPro: IPR000222; PP2C.
CC InterPro: IPR001932; PP2C_domain.
CC Pfam; PF00481; PP2C; 1.
CC SMART; SM00331; PP2C_SIG; 1.
CC SMART; SM00332; PP2CC; 1.
CC PROSITE; PS01032; PP2C; 1.
CC Hydrolase; Magnesium; Manganese; Multigene family;
KW Alternative splicing.
FT METAL 37 37 MANGANESE 1 (BY SIMILARITY).
FT METAL 38 38 MANGANESE 1 (BY SIMILARITY).
FT METAL 60 60 MANGANESE 1 AND 2 (BY SIMILARITY).
FT METAL 243 243 MANGANESE 2 (BY SIMILARITY).
FT METAL 286 286 MANGANESE 2 (BY SIMILARITY).
FT METAL 379 390 GAGDLEDSLVAL -> FYQPSTPYSDNVSYEWQT (IN
FT VARSPLIC ISOFORM BETA-MPP).
SQ SEQUENCE 390 AA; 42889 MW; D147615BC2FA140B CRC64;

Query Match      29.1%; Score 534; DB 1; Length 390;
Best Local Similarity 34.3%; Pred. No. 4.1e-34;
Matches 125; Conservative 54; Mismatches 109; Indels 76; Gaps 6;

QY 1 MGIVLCSPKTKTSEDDNAELRYGLSAMQGRWDSMEDAHKAILNVKNTST-SIFGIFD 59
DB 1 MGAFLDKPKTEKHAHAGCAGNGLRYGLSSMQGRVENEDAHAVVGIPHGLEDSWFFAYD 60

QY 60 GHGKLVAKFAKHLHQLKSEAYAKG-----LKASLEYSFLRMDWMKA 107
DB 61 GHAGSRVANYCSTHLLHEITNEDFRAADKSGFALPSPVENYKTIKRTGFLKIDEYMRNF 120

QY 108 SGWKLQSLSETSQDLKLGNGSSNAREDESYSYAVLTESNDSNLATKKHYSDFQ 167
DB 121 S-----DLRNGMDS----- 130

QY 168 GPIYGSTAVVALIRGNKLFVANAGDSRCIMSRGEAVNLSDHKPNLEHERKRIESAGGF 227
DB 131 ----GSTAVGMISPTHIYFINGDSRAVLCRNGQVCFSTQDHPKPCNPKMERIQNAGGS 186

QY 228 VHGGRVNGSNLNTRAIGDMFEKGRPDLPDPKQVVTCCPDVVEVDLPGDGFIVLACDGIW 287
DB 187 VMQVRVNGSLAVSRALGDYDKVCKGTEQLVSPPEVVEILRAEDEFVVLACDGIW 246

QY 288 DVMSQAQVDFVKSLPTTKTLSSLCEILDYCLSPTRQOECDNMSIIV-----QPKQ 343
DB 247 DVMSNEELCEFNLSREVSDDLNVNVCNVVDTCLHKGSR-----DNMSIVLCVFANAPKV 301

QY 344 SGVA 347
DB 302 SDEA 305

RESULT 15
P2CA_RAT      STANDARD;      PRT;      382 AA.
AC P20650;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Protein phosphatase 2c alpha isoform (EC 3.1.3.16) (PP2C-alpha) (IA)
DE (Protein phosphatase 1A).
GN PPM1A OR PPM1A OR PP2C1.
OS Rattus norvegicus (Rat).
```



```
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE=Kidney;
RX MEDLINE=89184515; PubMed=2538815;
RA Tamura S., Lynch K.R., Lerner J., Fox J., Yasui A., Kikuchi K.,
RT Suzuki Y., Tsukiki S.;
RL "Molecular cloning of rat type 2C (IA) protein phosphatase mRNA.";
CC Proc. Natl. Acad. Sci. U.S.A. 86:1796-1800(1989).
CC -1- FUNCTION: ENZYME WITH A BROAD SPECIFICITY.
CC -1- CATALYTIC ACTIVITY: A PHOSPHOPROTEIN + H(2)O = A PROTEIN +
CC ORTHOPHOSPHATE (THIS ENZYME IS SERINE/THREONINE SPECIFIC).
CC -1- COFACTOR: BINDS 2 MAGNESIUM OR MANGANESE IONS.
CC -1- SUBUNIT: MONOMER.
CC -1- SIMILARITY: BELONGS TO THE PP2C FAMILY.
CC -----
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CC -----
DR EMBL: J04503; AAA1917.1; -.
DR PIR: A32399; A32399.
DR HSSP: P35813; IA6Q.
DR InterPro: IPR000222; PP2C.
DR InterPro: IPR001932; PP2C_domain.
DR Pfam: PF00481; PP2C; 1.
DR SMART: SM00331; PP2C_SIG; 1.
DR SMART: SM00332; PP2C; 1.
DR PROSITE: PS01032; PP2C; 1.
DR Hydrolase; Magnesium; Manganese; Multigene family.
FT METAL 37 37 MANGANESE 1 (BY SIMILARITY).
FT METAL 38 38 MANGANESE 1 (BY SIMILARITY).
FT METAL 60 60 MANGANESE 1 AND 2 (BY SIMILARITY).
FT METAL 239 239 MANGANESE 2 (BY SIMILARITY).
FT METAL 282 282 MANGANESE 2 (BY SIMILARITY).
SQ SEQUENCE 382 AA; 42416 MW; C1C386E935374F89 CRC64;
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Query Match 28.4%; Score 522; DB 1; Length 382;
Best Local Similarity 34.1%; Pred. NO. 3.3e-33;
Matches 125; Conservative 59; Mismatches 109; Indels 74; Gaps 9;
QY 1 MGIVLCSPKTKTSEDDENALRYGLSAMOGWRDSMEDAHKAILNVKNTST-SIFGIFD 59
DB 1 MGAFLDKPRKEKNAOQGNGLRYGLSSMOGRVEMEDARTAVIGLPSGLETWSPFAVD 60
QY 60 GHGGLVAKFCAKHLHQELVKSEAYAG-----DLKASLEYSFLRMDEMKGASGWK 111
DB 61 GHAGSQVAKYCCHELLDHTNNQDF-KGSAGAPSVENVKNGIRTGFLIDEHMR----- 113
QY 112 ELQSLETSQDLKLGNGNSSNAREDDSDYSYAVLTESNDNSLNATKKHKYSDFGPIY 171
DB 114 -----VMSE-----KKH-----GADRS 125
QY 172 GSTAVVALIRGNKLFVANAGDSRCIMSRGAEAVNLSDHKPNLEHKKRIESAGGFVRHG 231
DB 126 GSTAVGLISQHTYFVINCDSRGLCRNKRKVHFFQDHDHKSPLNLEKRIQAGGSVMIQ 185
QY 232 RVNGSLNLTALIGDMEKRPDLPPDKQVVTCCPDVVEVDLG-PGDEFIVLACDGIWDM 290
DB 186 RVNGSLAVSRALGDFDKCVHGKGPTEQLVSPPEVHDIERSEEDDDQFILLACDGIWDM 245
QY 291 SSQAVDFVKSRLPTTKTLSSLCLEEILDYCLSPTRTQQEGCDNMSIIIV---QPKQSGV 346
DB 246 GNEELCDFVRSRLVETDLEKVCNEVVDCLYKGSR-----DNMSVILLICFPNPKVSAE 300
QY 347 AASSTD 353
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Db 301 AVKKEAE 307

Search completed: June 19, 2002, 08:47:49
Job time: 223 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 19, 2002, 08:42:46 ; Search time 20.94 seconds
(without alignments)
1619.844 Million cell updates/sec

Title: US-09-828-302-14
Perfect score: 1836
Sequence: 1 MGILCSPKTKYSEDDENA.....MSIIIVQPKSGVAASSSTD 353

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues
Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	973	53.0	357	2	T06308 protein phosphatase 2C homolog Flilc18.60 - Arabidopsis thaliana
2	967	52.7	355	2	H84643 probable protein p
3	635	34.6	370	2	S54297 protein phosphatase
4	616.5	33.6	300	2	A58004 phosphoprotein pho
5	608.5	33.1	414	2	S62462 protein phosphatase
6	606	33.0	348	2	E88434 protein T23f11.1
7	606	33.0	356	2	T25181 hypothetical prote
8	555.5	30.3	491	2	T16354 hypothetical prote
9	554.5	30.2	464	2	S05092 hypothetical prote
10	539	29.4	390	2	S65672 phosphoprotein pho
11	539	29.4	393	2	I49016 phosphoprotein pho
12	537	29.2	468	2	S39832 probable phosphor
13	534	29.1	390	2	S20392 phosphoprotein pho
14	534	29.1	397	2	JC2524 phosphoprotein pho
15	522	28.4	382	2	A32399 phosphoprotein pho
16	520	28.3	382	2	S2422 phosphoprotein pho
17	519	28.3	382	2	I53823 phosphoprotein pho
18	517	28.2	382	2	S22423 phosphoprotein pho
19	505.5	27.5	468	2	T21331 hypothetical prote
20	457	24.9	920	2	T08853 protein phosphatase
21	415.5	22.6	380	2	E84748 probable protein p
22	403.5	22.0	361	2	T45778 protein phosphatase
23	398.5	21.9	392	2	F84650 protein phosphatase
24	393.5	21.7	393	2	S48288 probable phosphor
25	363.5	19.8	442	2	B86209 protein phosphatase
26	358	19.5	348	2	T50783 protein phosphatase
27	357	19.4	362	2	F84695 probable protein p
28	355	19.3	511	2	F96752 protein phosphatase
29	354.5	19.3	359	2	T52337 phosphoprotein pho

30	354	19.3	434	2	T04263 phosphoprotein pho
31	353.5	19.3	396	2	T02483 probable protein p
32	350.5	19.1	388	2	C85323 protein phosphatase
33	346.5	18.9	386	2	T09019 phosphoprotein pho
34	346.5	18.9	389	2	T05095 hypothetical prote
35	343.5	18.7	347	2	A56058 phosphoprotein pho
36	341.5	18.6	281	2	S41854 phosphoprotein pho
37	334	18.2	399	2	S55457 phosphoprotein pho
38	330	18.0	405	2	F86206 hypothetical prote
39	327	17.8	383	2	T48018 protein phosphatase
40	326.5	17.8	381	2	T09640 protein phosphatase
41	326	17.8	406	2	A47492 protein F12A21.5
42	325	17.7	464	2	H96700 protein phosphatase
43	324.5	17.7	975	2	T08606 protein phosphatase
44	315.5	17.2	390	2	C84826 probable protein p
45	314	17.1	404	2	T00750

ALIGNMENTS

RESULT 1
T06308
protein phosphatase 2C homolog Flilc18.60 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cross)
C:Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 15-Jun-2001
C:Accession: T06308
R:Bevan, M.; Terry, N.; Ardiles, W.; Buysshaert, C.; Dasseville, R.; De Clerck, R.;
ewes, H.W.; Mayer, K.F.X.; Schueller, C.
submitted to the Protein Sequence Database, April 1999
A:Reference number: Z15589
A:Accession: T06308
A:Molecule type: DNA
A:Residues: 1-357 <BEV>
A:Cross-references: EMBL:AL049607; GSPDB:GN000062; ATSP:Flilc18.60
A:Experimental source: cultivar Columbia; BAC clone Flilc18
C:Genetics:
A:Gene: ATSP:Flilc18.60
A:Map position: 4
A:Introns: 39/3; 61/1; 97/2; 148/3; 190/3; 232/1; 257/3; 275/2; 293/3
C:Superfamily: human phosphoprotein phosphatase 1A

Query Match	53.0%	Score	973	DB	2	Length	357
Best Local Similarity	55.3%	Pred. NO.	1.2e-70				
Matches	192	Conservative	55	Mismatches	78	Indels	22
Gaps							3
QY	1	MGILCSPKTKDTSDENAELRYGLSAMQWRDSMEDAHKAILNVKNTSTFIFGFDG	60				
Db	1	MGILSTPKTKDFSEGDGENHKLRYGLSSMQWRASMEDAHAILDDDN--TSFLGVYDG	58				
QY	61	HGKLVAKFCAKHLHQEVLSKAYAKGLKASLEYSFLRMDMMKSGAKELQSLFETS	120				
Db	59	HGKLVYKFCYKHLHQVLSDEAYAGDVGTSIQKAFRRMDMMQGRWRELAIVLGIKI	118				
QY	121	SOLDKLGNG-----NSSNARDEDSYAVLITESNSNLATKKKYSDFQGIYGSTA	175				
Db	119	NKFSCHIEGLWSPRGDSANKPDA-----WAFEGPSHDFAGPNSGSTA	163				
QY	176	VVALIRGNLKFVANAGDSRCIMSRREAVNLSDHKPNLEHKKRISAGGVHGGRYNG	235				
Db	164	CVAVVRDKOLFVANAGDSRCVSRKNQAYNSRDHKPDLAEKIRLAKAGFIHAGRYNG	223				
QY	236	SLNLTRAIGDMFKRPDLPDQVVTCCPDVVEVDLPGDFEIVLACDGTWDMSSQAV	295				
Db	224	SLNLTRAIGDMFKRPDLPDQVVTCCPDVVEVDLPGDFEIVLACDGTWDMSSQAV	283				
QY	296	VDFVKSLRPTTKTSLSSCEILLDYCLSPTRQEGCDNMISIIIVQPK	342				
Db	284	VDFIHEQLNSETKLSVYCKEVLDRCLAPNTSGEGCDNMILVRFK	330				
RESULT	2						

H84643

probable protein phosphatase 2C [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 15-Jun-2001
C:Accession: H84643
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487
A:Accession: H84643
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-355 <SFO>
A:Cross-references: GB:AE002093; NID:g4559345; PIDN:AAD23006.1; GSPDB:GN00139
C:Genetics:
A:Gene: At2g25070
A:Map position: 2
C:Superfamily: human phosphoprotein phosphatase 1A

Query Match 52.7%; Score 967; DB 2; Length 355;
Best Local Similarity 53.3%; Pred. No. 3.5e-70;
Matches 188; Conservative 60; Mismatches 93; Indels 12; Gaps 2;
Qy 1 MGIIYLCSPKTDKTSSEDDENAEIRYGLSAMOGWRSDMEDAHKAILNVDKNTSTSIETFDG 60
Db 1 MGYLSSPKTKLSEGGDKRLGSLSMOGWRATMEDAHAILDLDD--DKYSFFGVYDG 58
Qy 61 HGGKLVAKFCAKHLHQEVKSEAYAKGDLKASLEYSLFRMDENMKMGASGKWLQSLLETS 120
Db 59 HGGKLVAKFCAKHLHQEVKSEAYAKGDLKASLEYSLFRMDENMKMGASGKWLQSLLETS 118
Qy 121 SOLDKLGNSSNAREDDSDSYAVLTESNDSNLATKKHKYSDFQGYSTAVVALI 180
Db 119 NFSGMTEGFTWSPRGD-----TNNQDPSPLEDGHPSDFGTSGCTACVALI 168
Qy 181 RGNKLFVANAGDSRCIMSRGAEAVNLSIDHKPNLEHERKRIESAGFVHGGRVNSLNT 240
Db 169 KDKLFVANAGDSRCVSRKSNYLSKDKHPDLEKEKERILKAGGFIHAGRINGSNLNT 228
Qy 241 RAIGDMFKGRDPLPPDKQVVTCCPDVVEVDLGPDEFLVACDGLWDMSSQAVDFVK 300
Db 229 RAIGDMFKQKFLPSEKQWTDADPDLNTIDLDDDFLVACDGLWDMSSQAVDFVK 288
Qy 301 SRLPPTTKTLLSLCEIILDYCLSPTRQEGCDNMSTIIIVOPKOSGVAASSSTD 353
Db 289 EQLAKETKLSVCEKVVDRCLAPDTATGEGCDNMSTIIIVQFKPNPSETEPED 341

RESULT 3
S54297
protein phosphatase 2C homolog - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C:Date: 15-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 15-Jun-2001
C:Accession: S54297; T40871
R:Shiozaki, K.; Russell, P.
EMBO J. 14, 492-502, 1995
A:Title: Counteractive roles of protein phosphatase 2C (PP2C) and a MAP kinase h
A:Reference number: S54297; MUID:95163582
A:Accession: S54297
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-370 <SHI>
A:Cross-references: EMBL:L34881; NID:g609655; PIDN:AAA67320.1; PID:g609656
R:Wedler, H.; Wambutt, R.; Lyne, M.; Rajandream, M.A.; Barrell, B.G.
submitted to the EMBL Data Library, September 1998
A:Reference number: Z21953
A:Accession: T40871
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-370 <WED>

A:Cross-references: EMBL:AL031579; PIDN:CAA20880.1; GSPDB:GN00068; SPDB:SPCC1223.11
A:Experimental source: strain 972h-; cosmid c1223
C:Genetics:
A:Gene: SPC1223.11
A:Map position: 3
C:Superfamily: human phosphoprotein phosphatase 1A

Query Match 34.6%; Score 635; DB 2; Length 370;
Best Local Similarity 41.6%; Pred. No. 2.1e-43;
Matches 144; Conservative 48; Mismatches 90; Indels 64; Gaps 8;
Qy 1 MGIIYLCSPKTDKTSSEDDENAEIRYGLSAMOGWRSDMEDAHKAILNVKNTS---TSIFG 56
Db 1 MGOTLSEPLVDKHSSSGGDRLHFGVSHMOGWRISMEDAHCALLNFTDSNSNPPTSFEG 60
Qy 57 IFDCHGKGLVAKFCAKHLHQEVKSE--AYAKGDLKASLEYSLFRMDENMKMGASGKWLQSL 115
Db 61 VFDCHGGRVAKYCRQHL-PDIIKSPSPFKGNYDALSGFLAAD----- 105
Qy 116 LEETSSQLDKLGNSSNAREDDSDSYAVLTESNDSNLATKKHKYSDFQGYSTAVVALI 175
Db 106 -----NALMQDR-----DMQEDPSGCTA 123
Qy 176 VVALIRGNK-LFVANAGDSRCIMSRGAEAVNLSIDHKPNLEHERKRIESAGFVHGGRVN 234
Db 124 TTALIVDQVIYCANAGDSRTVLGRKGTAEPLSFDHKPNNDVEKARITAGGFIDFGRVN 183
Qy 235 GSLNLTTRAIGDMFKGRDPLPPDKQVVTCCPDVVEVDLGPDEFLVACDGLWDMSSQ 294
Db 184 GSLALSRAIGDFEYKDDSLPPEKQIVTAPFDPVVIHINIDPDDEFLIACDGLWDCSSQ 243
Qy 295 VDFVKSRLPTTKTLLSLCEIILDYCLSPTRQ-QEGCDNMSTIIIV 339
Db 244 VVEFVRGIVAROSLEVICENLMDRCIASNSCSGIGCDNMTCIV 289

RESULT 4
A55804
phosphoprotein phosphatase (EC 3.1.3.16) 2c, membrane-bound - Paramesium tetraurelia
C:Species: Paramesium tetraurelia
C:Date: 23-Mar-1995 #sequence_revision 05-Apr-1995 #text_change 07-Dec-1999
C:Accession: A55804
R:Klump, S.; Hanke, C.; Donella-Deana, A.; Beyer, A.; Kellner, R.; Pinna, L.A.; Schu
J. Biol. Chem. 269, 32774-32780, 1994
A:Title: A membrane-bound protein phosphatase type 2C from Paramesium tetraurelia. Pu
A:Reference number: A55804; MUID:95105156
A:Accession: A55804
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-300 <KLJ>
A:Cross-references: GB:Z36985; NID:g537421; PID:ell92609; PID:g2654382
C:Genetics:
C:Keywords: phosphoric monoester hydrolase

Query Match 33.6%; Score 616.5; DB 2; Length 300;
Best Local Similarity 38.5%; Pred. No. 4.7e-42;
Matches 132; Conservative 61; Mismatches 99; Indels 51; Gaps 4;
Qy 1 MGIIYLCSPKTDKTSSEDDENAEIRYGLSAMOGWRSDMEDAHKAILNVKNTSTSIIFGFDG 60
Db 1 MGPYLSQPKRDKRTTTTGGKGVIFAASMOGWRNTMEDAH--IHRHDIITQDVSVEGFDG 58
Qy 61 HGGKLVAKFCAKHLHQEVKSEAYAKGDLKASLEYSLFRMDENMKMGASGKWLQSLLETS 120
Db 59 HGGREVAQFVEKHFVDELLANKNFKEEALKETFLKMDDELLTPGCKELNOYKAT- 117
Qy 121 SOLDKLGNSSNAREDDSDSYAVLTESNDSNLATKKHKYSDFQGYSTAVVALI 180
Db 118 -----DTDESVA-----GCTANVALI 133

RESULT 11
I49016
phosphoprotein phosphatase (EC 3.1.3.16) 1A - mouse
N; Alternate names: phosphoprotein phosphatase 1A beta-3
C; Species: Mus musculus (house mouse)
C; Date: 02-Jul-1996 #sequence_revision 1
C; Date: 02-Jul-1996 #sequence_revision 1
C; Accession: I49016; S56571; S39780; S39781
R; Hou, E.W.; Kawai, Y.; Miyasaka, H.; Li, S.S.
Biochem. Mol. Biol. Int. 32, 773-780, 1994
A; Title: Molecular cloning and expression of cDNAs encoding two isoforms of protein phosphatase 1A from mouse
A; Reference number: I49016; MUID:94313028
A; Accession: I49016
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Residues: 1-393 <RES>
A; Cross-references: EMBL:U09218; NID:g484099; PIDN:AAB60442.1; PID:g484100
A; Experimental source: tissue testis
R; Kato, S.; Terada, T.; Kobayashi, T.; Ohnishi, M.; Sasahara, Y.; Kusuda, K.; Yanagawa, A.
Arch. Biochem. Biophys. 318, 387-393, 1995
A; Title: Molecular cloning and expression of mouse Mg(2+)-dependent protein phosphatase 1A
A; Reference number: S56570; MUID:95251388

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Query Match      29.4%; Score 539; DB 2; Length 393;
Best Local Similarity 33.5%; Pred. No. 1.2e-35;
Matches 124; Conservative 58; Mismatches 112; Indels 76; Gaps 6;

QY 1 MGIYLCSPKTKTSEDDENAEIRGLSAMOGWRSDMEDAHKIILVNDKNTST-SIGIFD 59
DB 1 MGAFIDLPKTEKNAHAGAGNCLIRGLSMOGWRVEMEDAHTAVVGIPHGILDNWSFFAVID 60
QY 60 GHGKGLVAKFAKHLHGOVLKSEAYAKD-----LKASLEYSLFRMDEMKGKA 107
DB 61 GHAGSRVANYCSTHLEHITTNEDFRAADKSGSALEPSVESVKTGIRTFGLKIDVYMRNF 120
QY 108 SGWKELOSLEETSQOLDKLGNGNSSNAREDESIDYAVLTESDNLATKKHKYSDFQ 167
DB 121 S-----DLRNGMDRS----- 130
QY 168 GPIYGSTAVVALIRGNKLFVANAGDSRCIMSRRGAEVYNLSIDHKPNLEHBRKRIESAGGF 227
DB 131 ----GSTAVGVVWSPTHWYFINGCDGSRAVLRCNGQVCFSTQDHPKPCNPEVKERIQNAGGS 186
QY 228 VHGRVNGSLNLTFRAGIDMEFKRPPDLPPKQVVTCCPDVVEVDLPGDGFIVLACDGIW 287
DB 187 VMIQRVNGSLAVSRALGDYDKCVGDRGPTQLVSPPEYVEIVRAEEDFVWLACDGIW 246
QY 288 DVMSQAVDFVFKSRLPTTKTLLSCLIEILDYCLSPTRROEGCDNMSIIV----QPKQ 343
DB 247 DVMSNEELCEVKSRLVSESDLENVCNVWVDTCLHKGR-----DNMSVVLVCFSNAPKV 301
QY 344 SGVAASSTD 353
DB 302 SEEAVKRDSE 311

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RESULT 12
S39832
probable phosphoprotein phosphatase (EC 3.1.3.16) - yeast (*Saccharomyces cerevisiae*)
N:Alternate names: hypothetical protein YBL0511; hypothetical protein YBL0513; hypoth
C:Species: *Saccharomyces cerevisiae*
C:Date: 16-Dec-1993 #sequence_revision 09-Sep-1994 #text_change 15-Jun-2001
C:Accession: S39832; S45791; S37333
R:Scherens, B.; el Bakloury, M.; Vierendeels, F.; Dubois, E.; Messenguy, F.
Yeast 9, 1355-1371, 1993
A:Title: Sequencing and functional analysis of a 32 560 bp segment on the left arm of
A:Reference number: S39824; MUID:94205266
A:Accession: S39832
A:Molecule type: DNA

A:Residues: 1-468 <SCH>
A:Cross-references: EMBL:223261; NID:g313733; PIDN:CAA80791.1; PID:g313742
R:Experimental source: strain S288
R:Dubois, E.; El Bakoury, M.; Glausdorff, N.; Messenguy, F.; Pierard, A.; Scherens, B.;
submitted to the Protein Sequence Database, August 1994
A:Reference number: S45782
A:Accession: S45791
A:Molecule type: DNA
A:Residues: 1-468 <DUB>
A:Cross-references: SGD:S0000152; MIPS:YBL056w
A:Experimental source: strain S288
C:Genetics:
A:Gene: SGD:PTC3
A:Map position: 2L
A:Cross-references: SGD:S0000152; MIPS:YBL056w
A:Superfamily: human phosphoprotein phosphatase 1A
C:Keywords: phosphoric monoester hydrolase; serine/threonine-specific phosphatase

Query Match 29.2%; Score 537; DB 2; Length 468;
Best Local Similarity 38.8%; Pred. No. 2.2e-35;
Matches 135; Conservative 38; Mismatches 109; Indels 66; Gaps 9;

QY 1 MGIYLCSPKTDKTSDEDAENALRYGLSAMQWRDSMEDAH---KAILNVDRNTSTSTPGI 57
Db 1 MGQILSNPIIDKEHHSGTDCITAFGLCAMQWRMSMEDAHIVEPNLLAESDEEHLAFYGI 60
QY 58 FDHGKGLVAKFCAKHLHQLVLSKAYAKGDLKASLEYSFRLMD-EMMKASGKWLQSL 116
Db 61 FDHGGSVAEPFGCGKMSILKKQSFSGMLEQCLDTFTATVDLLKD----- 110
QY 117 EETSSQLDKLNGNSSNAREDESYSYAVLTESNDSNLATKKHKYSDFQPIYGSTAV 176
Db 111 -----EKL-----KDDHS-----GCTAT 123
QY 177 VALIRNK--LFVANAGDSRCIMSRGEAVNLSIDHKPNLEHERKRIESAGFVHGGRVN 234
Db 124 VILVSLKLLICANSGRSTVLSLGGSKAMSFPHKPTLLSEKSRIVAAOGFVEMDRVN 183
QY 235 GSLNLTTRAIGDMFEKGRPLDPDKQVVTCCPDVVEVDLG-PGDEFIVLACDGIWDMSSQ 293
Db 184 GNLALSRAIGDFEFKSNKLPQHPGVVTCVDPDIICHNLNYDEDEFVILACDGIWDMCLTSQ 243
QY 294 AVVDFVKSLRPLT-TKTLSSLCIEILDYCLSPPTTQOE-GCDNMSIIV 339
Db 244 ECVDLVHYGISQGNMTLSIDISSRIVDVCCSPPTTEGGIGCDNMSISIV 291

RESULT 13
S20392
phosphoprotein phosphatase (EC 3.1.3.16) 1A-2 - rat
N:Alternate names: protein phosphatase 2C.2
C:Species: Rattus norvegicus (Norway rat)
C:Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 15-Jun-2001
C:Accession: S20392
R:Wenk, J.; Trompeter, H.I.; Pettrich, K.G.; Cohen, P.T.W.; Campbell, D.G.; Mieskes, G.
FEBS Lett. 297, 135-138, 1992
A:Title: Molecular cloning and primary structure of a protein phosphatase 2C isoform.
A:Reference number: S20392; MUID:92201367
A:Accession: S20392
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-390 <WEN>
A:Cross-references: GB:S90449; NID:g247926; PIDN:AAB21898.1; PID:g247927
C:Superfamily: human phosphoprotein phosphatase 1A
C:Keywords: phosphoric monoester hydrolase; serine/threonine-specific phosphatase

Query Match 29.1%; Score 534; DB 2; Length 390;
Best Local Similarity 34.3%; Pred. No. 3e-35;
Matches 125; Conservative 54; Mismatches 109; Indels 76; Gaps 6;

QY 1 MGIYLCSPKTDKTSDEDAENALRYGLSAMQWRDSMEDAHKAILNVDRNTST-SIFGIFD 59
Db 1 MGAFLODKPKTEKHAHAGNGLRYGLSSMQWRVEMEDAHTAVVGIHGLDWSFFAVYD 60
QY 60 GHGKLVAKFCAKHLHQLVLSKAYAKG-----LKASLEYSLRMDENMKGA 107
Db 61 GHAGSRVANYCSTHLLHEITTFNEDFRAADKSGFALEPSVENVKVGTGRTGFLKIDYMRNF 120
QY 108 SGWKLQSLSEETSSQLDKLNGNSSNAREDESYSYAVLTESNDSNLATKKHKYSDFQ 167
Db 121 S-----DLRNGMDRS----- 130
QY 168 GPIYGSTAVVALIRGNKLFVANAGDSRCIMSRGEAVNLSIDHKPNLEHERKRIESAGGF 227
Db 131 ----GSTAVGMISPTHIYFINGDSRAVLCRNGQVCFSTQDHHKPCNPMKEKRIQNAAGS 186
QY 228 VHGRVNGSLNLTTRAIGDMFEKGRPLDPDKQVVTCCPDVVEVDLPGDGFIVLACDGIW 287
Db 187 VMTQRVNGSLAVSRALGDYDKCVDGKGPTEQLVSPPEVEYILRAEDEFVVLACDGIW 246

Query Match 29.1%; Score 534; DB 2; Length 397;
Best Local Similarity 34.3%; Pred. No. 3.1e-35;
Matches 125; Conservative 54; Mismatches 109; Indels 76; Gaps 6;

QY 1 MGIYLCSPKTDKTSDEDAENALRYGLSAMQWRDSMEDAHKAILNVDRNTST-SIFGIFD 59
Db 1 MGAFLODKPKTEKHAHAGNGLRYGLSSMQWRVEMEDAHTAVVGIHGLDWSFFAVYD 60
QY 60 GHGKLVAKFCAKHLHQLVLSKAYAKG-----LKASLEYSLRMDENMKGA 107
Db 61 GHAGSRVANYCSTHLLHEITTFNEDFRAADKSGFALEPSVENVKVGTGRTGFLKIDYMRNF 120
QY 108 SGWKLQSLSEETSSQLDKLNGNSSNAREDESYSYAVLTESNDSNLATKKHKYSDFQ 167
Db 121 S-----DLRNGMDRS----- 130
QY 168 GPIYGSTAVVALIRGNKLFVANAGDSRCIMSRGEAVNLSIDHKPNLEHERKRIESAGGF 227
Db 131 ----GSTAVGMISPTHIYFINGDSRAVLCRNGQVCFSTQDHHKPCNPMKEKRIQNAAGS 186
QY 228 VHGRVNGSLNLTTRAIGDMFEKGRPLDPDKQVVTCCPDVVEVDLPGDGFIVLACDGIW 287
Db 187 VMTQRVNGSLAVSRALGDYDKCVDGKGPTEQLVSPPEVEYILRAEDEFVVLACDGIW 246

A:Residues: 1-468 <SCH>
A:Cross-references: EMBL:223261; NID:g313733; PIDN:CAA80791.1; PID:g313742
R:Experimental source: strain S288
R:Dubois, E.; El Bakoury, M.; Glausdorff, N.; Messenguy, F.; Pierard, A.; Scherens, B.;
submitted to the Protein Sequence Database, August 1994
A:Reference number: S45782
A:Accession: S45791
A:Molecule type: DNA
A:Residues: 1-468 <DUB>
A:Cross-references: SGD:S0000152; MIPS:YBL056w
A:Experimental source: strain S288
C:Genetics:
A:Gene: SGD:PTC3
A:Map position: 2L
A:Cross-references: SGD:S0000152; MIPS:YBL056w
A:Superfamily: human phosphoprotein phosphatase 1A
C:Keywords: phosphoric monoester hydrolase; serine/threonine-specific phosphatase

Query Match 29.2%; Score 537; DB 2; Length 468;
Best Local Similarity 38.8%; Pred. No. 2.2e-35;
Matches 135; Conservative 38; Mismatches 109; Indels 66; Gaps 9;

QY 1 MGIYLCSPKTDKTSDEDAENALRYGLSAMQWRDSMEDAH---KAILNVDRNTSTSTPGI 57
Db 1 MGQILSNPIIDKEHHSGTDCITAFGLCAMQWRMSMEDAHIVEPNLLAESDEEHLAFYGI 60
QY 58 FDHGKGLVAKFCAKHLHQLVLSKAYAKGDLKASLEYSFRLMD-EMMKASGKWLQSL 116
Db 61 FDHGGSVAEPFGCGKMSILKKQSFSGMLEQCLDTFTATVDLLKD----- 110
QY 117 EETSSQLDKLNGNSSNAREDESYSYAVLTESNDSNLATKKHKYSDFQPIYGSTAV 176
Db 111 -----EKL-----KDDHS-----GCTAT 123
QY 177 VALIRNK--LFVANAGDSRCIMSRGEAVNLSIDHKPNLEHERKRIESAGFVHGGRVN 234
Db 124 VILVSLKLLICANSGRSTVLSLGGSKAMSFPHKPTLLSEKSRIVAAOGFVEMDRVN 183
QY 235 GSLNLTTRAIGDMFEKGRPLDPDKQVVTCCPDVVEVDLG-PGDEFIVLACDGIWDMSSQ 293
Db 184 GNLALSRAIGDFEFKSNKLPQHPGVVTCVDPDIICHNLNYDEDEFVILACDGIWDMCLTSQ 243
QY 294 AVVDFVKSLRPLT-TKTLSSLCIEILDYCLSPPTTQOE-GCDNMSIIV 339
Db 244 ECVDLVHYGISQGNMTLSIDISSRIVDVCCSPPTTEGGIGCDNMSISIV 291

RESULT 14
JC2524
phosphoprotein phosphatase (EC 3.1.3.16) 1A-beta - rat
N:Alternate names: magnesium-dependent protein phosphatase 1A; protein serine/threonin
C:Species: Rattus norvegicus (Norway rat)
C:Date: 17-May-1995 #sequence_revision 14-Jul-1995 #text_change 15-Jun-2001
C:Accession: JC2524
R:Schaefer, K.; Braun, T.
Biochem. Biophys. Res. Commun. 207, 708-714, 1995
A:Title: Monoclonal anti-flag antibodies react with a new isoform of rat Mg2+ depende
A:Reference number: JC2524; MUID:95169115
A:Accession: JC2524
A:Molecule type: mRNA
A:Residues: 1-397 <SCH>
A:Cross-references: GB:S74572; NID:g807067; PIDN:AAB33430.1; PID:g807068
A:Experimental source: brain
A:Superfamily: human phosphoprotein phosphatase 1A
C:Keywords: phosphoric monoester hydrolase; serine/threonine-specific phosphatase
F:206-213/Region: FLAG peptide

QY 288 DVMSQAVDFVKSRLPTTKTLLSLCEILDYCLSPTRQOEGCDNMSIIV---OPKQ 343
 Db 247 DVMSNEELCEFNRSRLVSDDLLENVCNWVVDICLHKGR-----DNMSIVLCFANAPKV 301

QY 344 SGVA 347
 Db 302 SDEA 305

RESULT 15

A32399
 phosphoprotein phosphatase (EC 3.1.3.16) 1A - rat
 N:Alternate names: protein phosphatase 2C
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 31-Jul-1989 #sequence_revision 31-Jul-1989 #text_change 15-Jun-2001
 C:Accession: A32399
 R:Tamura, S.; Lynch, K.R.; Lerner, J.; Fox, J.; Yasui, A.; Kikuchi, K.; Suzuki, Y.; Tsun
 Proc. Natl. Acad. Sci. U.S.A. 86, 1796-1800, 1989
 A:Title: Molecular cloning of rat type 2C (1A) protein phosphatase mRNA.
 A:Reference number: A32399; M0ID:89184515
 A:Accession: A32399
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-382 <TAM>
 A:Cross-references: GB:J04503; NID:q206312; PIDN:AAA41917.1; PID:q206313
 C:Superfamily: human phosphoprotein phosphatase 1A
 C:Keywords: liver; phosphoric monoester hydrolase; serine/threonine-specific phosphatase

Query Match 28.4%; Score 522; DB 2; Length 382;
 Best Local Similarity 34.1%; Pred. No. 2.7e-34;
 Matches 125; Conservative 59; Mismatches 109; Indels 74; Gaps 9;

QY 1 MGIYLCSPKTDKSEDDENAEIRYGLSAMQGRDSDAHKAILNVDKNTST-SIFGIFD 59
 Db 1 MGAFLDKPKMEKHNAQGGNGRLYGLSSMQGRVEMEDAHTAVIGLPSGLETWTFAYVD 60
 QY 60 GHGKLVAKFCAKHLHQLKSEAYAKG-----DLKASLEYSFLRMDEMKGASGWK 111
 Db 61 GHAGSQVAKYCCHELLDHTNNQDF-KGSAGAPSVENVKNGIRTGFLIDEHMR----- 113
 QY 112 ELQSEETSSQLDKLGNNGSSNAREDDSDYSYAVLTESDNSNLATKKHKYSDFQGPYI 171
 Db 114 -----VNSE-----KHH-----GADRS 125
 QY 172 GSTAVVALIRGNKLFVANAGDSRCIMSRGEAVNLSIDHKPNLEHERKRIESAGGFVHGG 231
 Db 126 GSTAVGLISFQHTYFVNCDSRGLCRNRKRVHFFQDHPKPNPLEKRIQNAGGSVMIQ 185
 QY 232 RVNGSLNLTRAIGDMFKGRPDLPDPKQVVTCCPDVVEVDLG-PGDEFIVLACDGIWDM 290
 Db 186 RVNGSLAVSRALGDFDYKCVHKGPTQLVSPPEVHDIERSEDDQFTILACDGIWDM 245
 QY 291 SSQAVDFVKSRLPTTKTLLSLCEILDYCLSPTRQOEGCDNMSIIV---OPKQSGV 346
 Db 246 GNEELCDFVRSRLVETDDLEKVCNEVVVDICLYKGR-----DNMSVILICFPNAPKVSNE 300
 QY 347 AASSTD 353
 Db 301 AVKKEAE 307

Search completed: June 19, 2002, 08:46:28
 Job time: 222 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 19, 2002, 08:41:40 ; Search time 13.29 Seconds
(without alignments)
648.776 Million cell updates/sec

Title: US-09-828-302-14
Perfect score: 1836
Sequence: 1 MGILCSPKTDKTSDDENA.....MSLIIVPKSGVAASSTD 353

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
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2: /cgn2.6/prodata/2/1aa/5B_COMB.pep:*
3: /cgn2.6/prodata/2/1aa/6A_COMB.pep:*
4: /cgn2.6/prodata/2/1aa/6B_COMB.pep:*
5: /cgn2.6/prodata/2/1aa/PCTUS_COMB.pep:*
6: /cgn2.6/prodata/2/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	643	35.0	546	3	US-08-935-855-20 Sequence 20, Appl
2	641.5	34.9	542	3	US-08-935-855-22 Sequence 22, Appl
3	538	29.3	478	2	US-08-873-093-1 Sequence 1, Appl
4	538	29.3	478	2	US-08-873-093-4 Sequence 4, Appl
5	534	29.1	390	2	US-08-873-093-3 Sequence 3, Appl
6	533.5	29.1	309	3	US-08-822-701-7 Sequence 7, Appl
7	533.5	29.1	309	3	US-08-935-855-7 Sequence 7, Appl
8	520	28.3	306	3	US-08-822-701-8 Sequence 8, Appl
9	520	28.3	306	3	US-08-935-855-8 Sequence 8, Appl
10	491.5	26.8	392	2	US-08-822-701-2 Sequence 2, Appl
11	491.5	26.8	392	3	US-08-935-855-2 Sequence 2, Appl
12	370.5	20.2	392	4	US-09-013-881-2 Sequence 2, Appl
13	341.5	18.6	281	3	US-08-822-701-9 Sequence 9, Appl
14	341.5	18.6	281	3	US-08-935-855-9 Sequence 9, Appl
15	326	17.8	314	3	US-08-822-701-10 Sequence 10, Appl
16	326	17.8	314	3	US-08-935-855-10 Sequence 10, Appl
17	156.5	8.5	504	2	US-08-752-891-2 Sequence 2, Appl
18	156.5	8.5	504	2	US-08-752-891-6 Sequence 6, Appl
19	156.5	8.5	504	2	US-09-144-178-2 Sequence 2, Appl
20	156.5	8.5	504	2	US-09-144-178-6 Sequence 6, Appl
21	156.5	8.5	504	4	US-09-406-854-2 Sequence 2, Appl
22	156.5	8.5	504	4	US-09-406-854-6 Sequence 6, Appl
23	97.5	5.3	15281	2	US-08-471-119A-2 Sequence 2, Appl
24	90	4.9	707	2	US-08-949-941B-2 Sequence 2, Appl
25	89	4.8	802	2	US-08-007-107-4 Sequence 4, Appl
26	88.5	4.8	1477	1	US-08-038-682-4 Sequence 4, Appl
27	88.5	4.8	1477	1	US-08-302-832-4 Sequence 4, Appl

28	88.5	4.8	1477	2	US-08-530-198-4	Sequence 4, Appl
29	88.5	4.8	1477	2	US-08-469-880-4	Sequence 4, Appl
30	88.5	4.8	1477	2	US-08-728-470-4	Sequence 4, Appl
31	88.5	4.8	1477	2	US-08-617-697-4	Sequence 4, Appl
32	88.5	4.8	1477	4	US-08-719-641-4	Sequence 4, Appl
33	88.5	4.8	2285	4	US-09-308-375-2	Sequence 2, Appl
34	88	4.8	3111	2	US-08-460-309-4	Sequence 4, Appl
35	88	4.8	3111	2	US-08-125-077-4	Sequence 4, Appl
36	88	4.8	3898	4	US-08-750-717-2	Sequence 2, Appl
37	86	4.7	3898	2	US-08-876-991-2	Sequence 2, Appl
38	86	4.7	3898	2	US-09-059-853-2	Sequence 2, Appl
39	84	4.6	793	1	US-08-188-228-54	Sequence 54, Appl
40	84	4.6	793	1	US-08-332-643-48	Sequence 48, Appl
41	84	4.6	793	1	US-08-332-638-54	Sequence 54, Appl
42	83	4.5	484	1	US-08-030-096-8	Sequence 8, Appl
43	82	4.5	546	2	US-08-942-423-4	Sequence 4, Appl
44	82	4.5	546	4	US-08-630-915A-14	Sequence 14, Appl
45	82	4.5	687	2	US-08-540-804-4	Sequence 4, Appl

ALIGNMENTS

RESULT 1
US-08-935-855-20
; Sequence 20, Application US/08935855
; Patent No. 6066485
; GENERAL INFORMATION:
; APPLICANT: Guthridge, Mark
; APPLICANT: Basilico, Claudio
; TITLE OF INVENTION: NOVEL GROWTH FACTOR INDUCIBLE
; TITLE OF INVENTION: SERINE/THREONINE PHOSPHATASE, FIN13
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/935,855
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 1049-1-002 CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 546 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; US-08-935-855-20

Query Match 35.0%; Score 643; DB 3; Length 546;
Best Local Similarity 32.7%; Pred. No. 9.3e-61;
Matches 165; Conservative 60; Mismatches 112; Indels 168; Gaps 9;


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; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/873,093
; FILING DATE: Filed Herewith
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0319 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 478 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: THPILE01
; CLONE: 13177
; US-08-873-093-1
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Query Match 29.3%; Score 538; DB 2; Length 478;
Best Local Similarity 34.6%; Pred. No. 1.7e-49;
Matches 128; Conservative 57; Mismatches 109; Indels 76; Gaps 7;

QY 1 MGIYLCSPKTKTSEDDENAEALRYGLSAMQGRWDSMEDAHKALLNVYDKNTST-SIFGIFD 59
Db 1 MGAFLDPKTEKHNAHGAGNGLRYGLSSMQGRVEMEDAHTAVVGIPHGLEDWSEFFAYVD 60

QY 60 GHGKLVAKFCAKHLHQEVLLKSEAY-AKGDLKASLEYS-----FLRMDMMKGA 107
Db 61 GHAGSRVANYCSTHLLHETITNEDFRAAGKSGSALESLVENKNGIRTGFLKIDYMRNF 120

QY 108 SGWKELOSLEETSSQLDKLNGNSSNAREDDSDYSYAVLTESNDSNLATKKHYSDFQ 167
Db 121 S-----DLRNGMDRS----- 130

QY 168 GPIYGSTAVVALIRGNKLFVANAGDSRCIMSRGEAVNLSIDHKPNLEHERKRIESAGGF 227
Db 131 ----GSTAVGVMISPKHIYFINGDSRAVLYRNGQVCFSTQDHKPCNPREKERIQNAGS 186

QY 228 VHGRVNGSLNLTIRAIGDMFEKGRPDLPDKQVVTCCPDVVEVDLGPQDEFIVLACDGIW 287
Db 187 VMIQVRNGSLAVSRALGDYDKCVGDKGPTQQLVSPPEVYEILRAEDEFIILACDGIW 246

QY 288 DVMSQAVDFVKSRLPPTTKTSLCEEILDYCLSPTTTQOECGDNMSIIV----QPKQ 343
Db 247 DVMSNEELCEYKSRLEVSDDLENVCNVWVYDTCLHKGSR-----DNMSIVLVCFNSAPKV 301

QY 344 SGVAASSTD 353
Db 302 SDEAVKKDSE 311
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RESULT 4
US-08-873-093-4
; Sequence 4, Application US/08873093
; Patent No. 5853997
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Goli, Surya K.
; APPLICANT: Lal, Preeti
; APPLICANT: Corley, Neil C.
; APPLICANT: Zhang, Hong
; TITLE OF INVENTION: NEW PROTEIN PHOSPHATASE
```

```
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/873,093
; FILING DATE: Filed Herewith
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0319 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 478 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: Genbank
; CLONE: 1452526
; US-08-873-093-4
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Query Match 29.3%; Score 538; DB 2; Length 478;
Best Local Similarity 34.6%; Pred. No. 1.7e-49;
Matches 128; Conservative 57; Mismatches 109; Indels 76; Gaps 7;

QY 1 MGIYLCSPKTKTSEDDENAEALRYGLSAMQGRWDSMEDAHKALLNVYDKNTST-SIFGIFD 59
Db 1 MGAFLDPKTEKHNAHGAGNGLRYGLSSMQGRVEMEDAHTAVVGIPHGLEDWSEFFAYVD 60

QY 60 GHGKLVAKFCAKHLHQEVLLKSEAY-AKGDLKASLEYS-----FLRMDMMKGA 107
Db 61 GHAGSRVANYCSTHLLHETITNEDFRAAGKSGSALESLVENKNGIRTGFLKIDYMRNF 120

QY 108 SGWKELOSLEETSSQLDKLNGNSSNAREDDSDYSYAVLTESNDSNLATKKHYSDFQ 167
Db 121 S-----DLRNGMDRS----- 130

QY 168 GPIYGSTAVVALIRGNKLFVANAGDSRCIMSRGEAVNLSIDHKPNLEHERKRIESAGGF 227
Db 131 ----GSTAVGVMISPKHIYFINGDSRAVLYRNGQVCFSTQDHKPCNPREKERIQNAGS 186

QY 228 VHGRVNGSLNLTIRAIGDMFEKGRPDLPDKQVVTCCPDVVEVDLGPQDEFIVLACDGIW 287
Db 187 VMIQVRNGSLAVSRALGDYDKCVGDKGPTQQLVSPPEVYEILRAEDEFIILACDGIW 246

QY 288 DVMSQAVDFVKSRLPPTTKTSLCEEILDYCLSPTTTQOECGDNMSIIV----QPKQ 343
Db 247 DVMSNEELCEYKSRLEVSDDLENVCNVWVYDTCLHKGSR-----DNMSIVLVCFNSAPKV 301

QY 344 SGVAASSTD 353
Db 302 SDEAVKKDSE 311
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RESULT 5
US-08-873-093-3
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; Sequence 3, Application US/08873093
; Patent No. 5853997
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Goli, Surya K.
; APPLICANT: Lal, Preeti
; APPLICANT: Corley, Neil C.
; APPLICANT: Zhang, Hong
; TITLE OF INVENTION: NEW PROTEIN PHOSPHATASE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/873,093
; FILING DATE: Filed Herewith
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0319 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 390 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 1247927
; US-08-873-093--3

Query Match          29.1%; Score 534; DB 2; Length 390;
Best Local Similarity 34.3%; Pred No. 3.3e-49;
Matches 125; Conservative 54; Mismatches 109; Indels 76; Gaps 6;

Qy 1 MGIYLCSPKTDKTSDDENAEALRYGLSAMQGRWDSMEDAHKAILNVKNTST-SIFGIFD 59
Db 1 MGAFLDKPKTEKHAHAGNGLRYGLSSMQGRVEMEDAHTAVVGIPHGLEDWSFFAYVD 60

Qy 60 GHGKLVAKCAKHLHQLKSEAYAKG-----LKASLE-----YSLRWDEMMKGAS 107
Db 61 GHAGSRVANTCSTHLLDHTITNEDFRAADKSGFALPSPVENVKTGIRGFLKIDEYMRNF 120

Qy 108 SGWKELOSLEETSOLDKLGNGSSNAREDDSDYSYAVLTESNDSNLATKKHKYSDFQ 167
Db 121 S-----DLRNGMDRS----- 130

Qy 168 GPIYGTAVVALLIRGNKLFVANAGDSRCIMSRGEAVNLSIDHKPNLEHERKRIESAGGF 227
Db 131 -----GSTAVGMISPTTHIVFINGDSRAVLCRNGQVCFSTQDKHKPCNPKERIQNAGGS 186

Qy 228 VHGRVNGSLNLTARIGDMEFKGRPDLPDKQVVTCCPDWVDVLGPGDEFIVLACDGIW 287
Db 187 VMIOVRNGSLAVSRALGDYKCDGKGTQELVSPPEVYELRAEDEFVVLACDGIW 246

Qy 288 DVMSNVAVDFVKSRPLPTTKTSLSLCEEILDYCLSTPTTRQCGCDNMSTIIIV-----QPKQ 343
Db 288 DVMSNEELCEFNVRLEVSDDLENVCNVWVDTCLHKGSR-----DNMSIVLCFANAPXV 301

; Sequence 7, Application US/08822701
; Patent No. 5976853
; GENERAL INFORMATION:
; APPLICANT: Guthridge, Mark
; APPLICANT: Basilico, Claudio
; TITLE OF INVENTION: NOVEL GROWTH FACTOR INDUCIBLE
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/822,701
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 1049-1-002 N
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 309 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEetical: NO
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; ORGANISM: Mus musculus
; US-08-822-701-7

Query Match          29.1%; Score 533.5; DB 2; Length 309;
Best Local Similarity 34.7%; Pred. No. 2.6e-49;
Matches 125; Conservative 56; Mismatches 104; Indels 75; Gaps 7;

Qy 1 MGIYLCSPKTDKTSDDENAEALRYGLSAMQGRWDSMEDAHKAILNVKNTST-SIFGIFD 59
Db 1 MGAFLDKPKTEKHAHAGNGLRYGLSSMQGRVEMEDAHTAVVGIPHGLEDWSFFAYVD 60

Qy 60 GHGKLVAKCAKHLHQLKSEAYAKG-----LKASLE-----YSLRWDEMMKGAS 108
Db 61 GHAGSRVANTCSTHLLDHTITNEDFRAADKSGFALPSPVENVKTGIRGFLKIDEYMRNF 120

Qy 109 GWKELOSLEETSOLDKLGNGSSNAREDDSDYSYAVLTESNDSNLATKKHKYSDFQ 168
Db 121 -----DLRNGMDRS----- 129

Qy 169 PIYGTAVVALLIRGNKLFVANAGDSRCIMSRGEAVNLSIDHKPNLEHERKRIESAGGFV 228
Db 169 DVMSNEELCEFNVRLEVSDDLENVCNVWVDTCLHKGSR-----DNMSIVLCFANAPXV 301
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Db 130 --GSTAVGVMSPTHTMYFINCGDSRAVLCRNGQVCFSTQDHPKPCNPVEKERIQNAGGSV 186
 Qy 229 HGRVNGSLNLTARIGDMFKGRPDLPDPKQVVTCCPDVVEVDLPGDFEIVLACDGIWD 288
 Db 187 MIQRVNGSLAVSRALGDYDKVDGKGPTEQLVSPPEVEIVRAEEDFEVVLACDGIWD 246
 Qy 289 VMSQAVVDVFKSRPLPTTKTLSSLCBEILDYCLSPTRQOEGCDNMSIIIV-----QPKOS 344
 Db 247 VMSNEELCEFKSRLEVSDDLENVCMVWVDTCLHKGSR-----DNMSVVLVCFSNAPKVS 301

RESULT 7
 US-08-935-855-7
 ; Sequence 7, Application US/08935855
 ; Patent No. 6066485
 ; GENERAL INFORMATION:
 ; APPLICANT: Guthridge, Mark
 ; APPLICANT: Basilio, Claudio
 ; TITLE OF INVENTION: NOVEL GROWTH FACTOR INDUCIBLE
 ; TITLE OF INVENTION: SERINE/THREONINE PHOSPHATASE, FIN13
 ; NUMBER OF SEQUENCES: 22
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: David A. Jackson, Esq.
 ; STREET: 411 Hackensack Ave, Continental Plaza, 4th
 ; CITY: Hackensack
 ; STATE: New Jersey
 ; COUNTRY: USA
 ; ZIP: 07601
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/935,855
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Jackson Esq., David A.
 ; REGISTRATION NUMBER: 26,742
 ; REFERENCE/DOCKET NUMBER: 1049-1-002 CIP
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 201-487-5800
 ; TELEFAX: 201-343-1684
 ; INFORMATION FOR SEQ ID NO: 7:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 309 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; HYPOTHETICAL: NO
 ; FRAGMENT TYPE:
 ; ORIGINAL SOURCE:
 ; ORGANISM: Mus musculus
 ;
 ; US-08-935-855-7

Query Match 29.1%; Score 533.5; DB 3; Length 309;
 Best Local Similarity 34.7%; Pred. No. 2.6e-49;
 Matches 125; Conservative 56; Mismatches 104; Indels 75; Gaps 7;

Qy 1 MGIYLCSPKTDKTSSEDDENAEALRYGLSAMQWRDSDMEDAHKAILNVDRNTST-SIFGIFD 59
 Db 1 MGAFLDKPKTEKINAGAGNGLRYGLSSMQGWRVEMEDAHAVGIPHGLDNWSPFAYD 60
 Qy 60 GHGKLVAKFCAKHLHQEVLSKAYAKG-----LKASLE-----YSFLRDEMAMKAS 108
 Db 61 GHAGSRVANYCSTHLLHITNEDFRADKSGSALEPSVESYKGTGTGLKIDETWRNFS 120
 Qy 109 GWKELQSLETSQDLKLGNGNSSNAREDDSDYSYAVLTESDNLATKHKHYSDFQG 168

Db 121 -----DLRNGMDRS----- 129
 Qy 169 PIYGSTAVVALIRGNKLFVANAGDSCIMSRCEAVNLSIDHKPNLEHERKRIESAGGFV 228
 Db 130 --GSTAVGVMSPTHTMYFINCGDSRAVLCRNGQVCFSTQDHPKPCNPVEKERIQNAGGSV 186
 Qy 229 HGRVNGSLNLTARIGDMFKGRPDLPDPKQVVTCCPDVVEVDLPGDFEIVLACDGIWD 288
 Db 187 MIQRVNGSLAVSRALGDYDKVDGKGPTEQLVSPPEVEIVRAEEDFEVVLACDGIWD 246
 Qy 289 VMSQAVVDVFKSRPLPTTKTLSSLCBEILDYCLSPTRQOEGCDNMSIIIV-----QPKOS 344
 Db 247 VMSNEELCEFKSRLEVSDDLENVCMVWVDTCLHKGSR-----DNMSVVLVCFSNAPKVS 301

RESULT 8
 US-08-822-701-8
 ; Sequence 8, Application US/08822701
 ; Patent No. 5976853
 ; GENERAL INFORMATION:
 ; APPLICANT: Guthridge, Mark
 ; APPLICANT: Basilio, Claudio
 ; TITLE OF INVENTION: NOVEL GROWTH FACTOR INDUCIBLE
 ; TITLE OF INVENTION: SERINE/THREONINE PHOSPHATASE, FIN13
 ; NUMBER OF SEQUENCES: 18
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: David A. Jackson, Esq.
 ; STREET: 411 Hackensack Ave, Continental Plaza, 4th
 ; CITY: Hackensack
 ; STATE: New Jersey
 ; COUNTRY: USA
 ; ZIP: 07601
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/822,701
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Jackson Esq., David A.
 ; REGISTRATION NUMBER: 26,742
 ; REFERENCE/DOCKET NUMBER: 1049-1-002 N
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 201-487-5800
 ; TELEFAX: 201-343-1684
 ; INFORMATION FOR SEQ ID NO: 8:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 306 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; HYPOTHETICAL: NO
 ; FRAGMENT TYPE:
 ; ORIGINAL SOURCE:
 ; ORGANISM: Rattus
 ;
 ; US-08-822-701-8

Query Match 28.3%; Score 520; DB 2; Length 306;
 Best Local Similarity 34.6%; Pred. No. 7.3e-48;
 Matches 125; Conservative 58; Mismatches 104; Indels 74; Gaps 9;

Qy 1 MGIYLCSPKTDKTSSEDDENAEALRYGLSAMQWRDSDMEDAHKAILNVDRNTST-SIFGIFD 59
 Db 1 MGAFLDKPKTEKINAGAGNGLRYGLSSMQGWRVEMEDAHAVGIPHGLDNWSPFAYD 60
 Qy 60 GHGKLVAKFCAKHLHQEVLSKAYAKG-----DLKASLEYSFLRDEMAMKASGK 111

Db 61 GHAGSQVAKYCECHLHDTNNQDF-KGSAGAPSVENKNGIRTFLEIDEHMR-----113
Qy 112 ELQSLEETSSQLDKLNGNSSNAREDESYSYAVLTESNDSNLATKKHKYSDFOGPIY 171
Db 114 -----VKSE-----KKH-----GADRS 125
Qy 172 GSTAVVALIRGNKLFVANAGDSRCIMSRGCEAVNLSIDHKPNLEHKKRRIESAGGPFVHGG 231
Db 136 GSTAVGLISPOHTYFNCGDSRGLLRNKKVHFFTDHKKPSNPLEKRIQNAGGSVMIQ 185
Qy 232 RVNGSLNLTGAIGDMFKGRPDLPDKQVVTCCPDVVEVDLG-PGDEFIVLACDGIWDVM 290
Db 186 RVNGSLAVSRALGDFDKCVHGKPTQLVSPPEVHDIERSEDDQFIILACDGIWDVM 245
Qy 291 SSQAVVDFVKSRLPTTTLSSLCBEILDYCLSPTRQOEGCDNMSIIV-----OPKQSV 346
Db 246 GNEELCDFVRSRLVTDLEKVCNEVVDTCLYKGSR-----DNMSVILICFPNAPKVSAAE 300
Qy 347 A 347
Db 301 A 301
RESULT 9
US-08-935-855-8
; Sequence 8, Application US/08935855
; Patent No. 6066485
; GENERAL INFORMATION:
; APPLICANT: Guthridge, Mark
; APPLICANT: Basilico, Claudio
; TITLE OF INVENTION: NOVEL GROWTH FACTOR INDUCIBLE
; TITLE OF INVENTION: SERINE/THREONINE PHOSPHATASE, FIN13
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; STREET: Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 1049-1-002 CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 306 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; ORGANISM: Rattus
US-08-935-855-8

Query Match 28.3%; Score 520; DB 3; Length 306;
Best Local Similarity 34.6%; Pred. No. 7.3e-48;

Matches 125; Conservative 58; Mismatches 104; Indels 74; Gaps 9;
Qy 1 MGILYCPKTDKTSSEDDENAEELRYGLSAMOGWRSDMEDAHKALNVKNTST-SIFGIFD 59
Db 1 MGAELDRPKMEKHNAOQNGRLYGLSSMGWRVEMEDAHTAVIGLPSGLETSFPAVD 60
Qy 60 GHGKLVAKCAKHLHGVLEKSEAYAKG-----DLKASLEYSFLRDEMMKASGAK 111
Db 61 GHAGSQVAKYCECHLHDTNNQDF-KGSAGAPSVENKNGIRTFLEIDEHMR-----113
Qy 112 ELQSLEETSSQLDKLNGNSSNAREDESYSYAVLTESNDSNLATKKHKYSDFOGPIY 171
Db 114 -----VKSE-----KKH-----GADRS 125
Qy 172 GSTAVVALIRGNKLFVANAGDSRCIMSRGCEAVNLSIDHKPNLEHKKRRIESAGGPFVHGG 231
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Qy 232 RVNGSLNLTGAIGDMFKGRPDLPDKQVVTCCPDVVEVDLG-PGDEFIVLACDGIWDVM 290
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Qy 291 SSQAVVDFVKSRLPTTTLSSLCBEILDYCLSPTRQOEGCDNMSIIV-----OPKQSV 346
Db 246 GNEELCDFVRSRLVTDLEKVCNEVVDTCLYKGSR-----DNMSVILICFPNAPKVSAAE 300
Qy 347 A 347
Db 301 A 301
RESULT 10
US-08-822-701-2
; Sequence 2, Application US/08822701
; Patent No. 5976853
; GENERAL INFORMATION:
; APPLICANT: Guthridge, Mark
; APPLICANT: Basilico, Claudio
; TITLE OF INVENTION: NOVEL GROWTH FACTOR INDUCIBLE
; TITLE OF INVENTION: SERINE/THREONINE PHOSPHATASE, FIN13
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; STREET: Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 1049-1-002 N
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 392 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO

FRAGMENT TYPE: N-terminal
US-08-822-701-2

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US-08-935-855-2
; Sequence 2, Application US/08935855
; Patent No. 6066485
; GENERAL INFORMATION:
; APPLICANT: Guthridge, Mark
; APPLICANT: Basillico, Claudio
; TITLE OF INVENTION: NOVEL GROWTH FACTOR INDUCIBLE
; TITLE OF INVENTION: SERINE/THREONINE PHOSPHATASE, FIN13
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PC-DOS/MS-DOS
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/935,855
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 1049-1-002 CIP
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 392 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; FRAGMENT TYPE: N-terminal
US-08-935-855-2

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Best Local Similarity 46.0%; Pred. No. 1.3e-44;

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RESULT 12
US-09-013-881-2
; Sequence 2, Application US/09013881
; Patent No. 6132964
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Lal, Preeti
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl J.
; APPLICANT: Shah, Purvi
; TITLE OF INVENTION: HUMAN HYDROLASE-LIKE MOLECULES
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/013,881
; FILING DATE: HERewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: BILLINGS, LUCY J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0470 US
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 392 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: KIDNOT02
; CLONE: 195647
US-09-013-881-2

Query Match 20.2%; Score 370.5; DB 4; Length 392;
Best Local Similarity 28.0%; Pred. No. 1.6e-31;

Search completed: June 19, 2002, 08:44:02
Job time: 142 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 19, 2002, 08:39:45 ; Search time 32.57 Seconds
(without alignments)
1203.839 Million cell updates/sec

Title: US-09-828-302-14
Perfect score: 1836
Sequence: 1 MGIIYLCSPKTKTSEDDENA.....MSIIIVPKSQGVAASSSTD 353

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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7	764	41.6	315	21	AA43239
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9	764	41.6	339	21	AA43239
10	669.5	36.5	438	22	AA43239
11	655.5	35.7	662	22	AA43239

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PR 30-APR-1999; 99US-0132407.
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PR 07-MAY-1999; 99US-0132487.
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PR 27-MAY-1999; 99US-0136392.
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KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
OS Arabidopsis thaliana.
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XX EP1033405-A2.
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hybridisation assay; genetic mapping; gene expression control; promoter;
termination sequence.
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PR 28-OCT-1999; 99US-0161992.
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Query Match 41.6%; Score 764; DB 21; Length 315;
Best Local Similarity 50.9%; Pred. No. 1.6e-62;
Matches 149; Conservative 51; Mismatches 83; Indels 10; Gaps 1;
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Qy 301 SRLPTTKTLSSLCEEILDYCLSPTRQOEGCDNMNIIIVQPKSGVAASSSTD 353
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Db 249 eqksetklstvcckvvdrclapdtatgdcgmntllilvqfkkpnpseteped 301

RESULT 8
AAG11785
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DE Arabidopsis thaliana protein fragment SEQ ID NO: 10638.
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KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence.
OS Arabidopsis thaliana.
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PN EP1033405-A2.
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PD 06-SEP-2000.
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PF 25-FEB-2000; 2000EP-0301439.
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PR 25-AUG-1999;	99US-0150566.		
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PR 30-AUG-1999;	99US-0151303.		
PR 31-AUG-1999;	99US-0151438.		
PR 01-SEP-1999;	99US-0151930.		

AA82980 standard; Protein; 438 AA.
AA82980;
21-DEC-2001 (first entry)
Trichoderma reesei PTC2, involved in unfolded protein response.
PTC2; phosphatase; unfolded protein response; protein secretion.
Trichoderma reesei.
WO200172783-A2.
04-OCT-2001.
23-MAR-2001; 2001WO-US09401.
24-MAR-2000; 2000US-0534692.
(GEMV) GENENCOR INT INC.
Penttila ME, Ward M, Wang H, Valkonen MJ, Saloheimo MLA;
WPI; 2001-626252/72.
N-PSDB; AAH26935.
Increasing secretion of heterologous proteins e.g. lipase and cellulase
in eukaryotic cells useful in industry to increase production and
facilitate purification, by inducing an elevated unfolded protein
response -
Claim 66; Fig 25; 89pp; English.
The present sequence is that of Trichoderma reesei PTC2, a protein
phosphatase that dephosphorylates IRE1 protein and regulates the
unfolded protein response (UPR). The invention provides methods
for increasing the secretion of a heterologous protein in a cell by
inducing an elevated UPR. This can be achieved by modulating the
activity of HAC1 (or haca), PTC2/B or IRE1 in the cell. The cell
from which the protein is secreted can be any cell having an UPR,
such as mammalian cells, insect cells, yeast and filamentous fungi.
The protein of interest can be any secreted protein such as a
therapeutic protein or an industrial enzyme, e.g. lipase, cellulase,
endoglucanase-H, protease, carbohydratase, reductase, oxidase,
isomerase, transferase, kinase, phosphatase, alpha-amylase,
glucoamylase, lignocellulose hemicellulase, pectinase and ligninase
(claimed).
Sequence 438 AA;
Query Match 36.5%; Score 669.5; DB 22; Length 438;
Best Local Similarity 43.1%; Pred. No. 1.5e-53;
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DB 61 sffgvfdghgkvalfagenhniufkqesfkgdyagglkgdglatdr----- 110
QY 113 LOSLETSQDLKLGNGSSNAREDESIDYAVLTESQNSLATKKHKYSDFOGPIYG 172
DB 111 -----all-----ndp-----kyye-----evsg 124
QY 173 STAVVALIRGNLKFVANAGDSRRCIMSRGEAYNLSIDHKPNLEHRRKTESAGGFVHGGR 232
DB 125 ctacvtliagnklyvanagdsrsvlgikrakplndhkpqleteknritaaggfvdgr 184
QY 233 VNGSLNLTIRAIGMEFKRPDLPPKQVVTCCPDVVEVDLPGDEFIVLACDGIWDVWSS 292

DB 185 vngnlalstraigdfefkksaelspengivtafpdvhelteedeflviacdgiwdcqss 244
QY 293 QAVVDFVKSRLPTTKTLSSLCBEILDYCLSPTRQ-OEGCDNMSSIIIV 339
DB 245 gavvefvrriagaakqldkicemmmncinlasnsetggvgcdnmtmvil 292
RESULT 11
ABB59430
ID ABB59430 standard; Protein; 662 AA.
XX
AC ABB59430;
XX
DT 26-MAR-2002 (first entry)
XX
DE Drosophila melanogaster polypeptide SEQ ID NO 5082.
XX
KW Drosophila; developmental biology; cell signalling; insecticide;
KW pharmaceutical.
XX
OS Drosophila melanogaster.
XX
PN WO200171042-A2.
XX
PD 27-SEP-2001.
XX
PF 23-MAR-2001; 2001WO-US09231.
XX
PR 23-MAR-2000; 2000US-191637P.
XX
PR 11-JUL-2000; 2000US-0614150.
XX
PA (PEKE) PE CORP NY.
XX
PI Venter JC, Adams M, Li PWD, Myers EW;
XX
WPI; 2001-656860/75.
DR N-PSDB; ABL03533.
XX
PT New isolated nucleic acid detection reagent for detecting 1000 or more
genes from Drosophila and for elucidating cell signalling and cell-cell
interactions -
XX
PS Disclosure; SEQ ID NO 5082; 21pp + Sequence Listing; English.
XX
CC The invention relates to an isolated nucleic acid detection reagent
capable of detecting 1000 or more genes from Drosophila. The invention is
useful in developmental biology and in elucidating cell signalling and
cell-cell interactions in higher eukaryotes for the development of
insecticides, therapeutics and pharmaceutical drugs. The invention
discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
sequences (ABL01840-ABL0175) and the encoded proteins
(ABB57737-ABB72072).
CC The sequence data for this patent did not form part of the printed
specification, but was obtained in electronic format directly from WIPO
at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 662 AA;

Query Match 35.7%; Score 655.5; DB 22; Length 662;
Best Local Similarity 28.6%; Pred. No. 5.3e-52;
Matches 167; Conservative 68; Mismatches 116; Indels 233; Gaps 11;

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DB 1 mgaylshpkcdktsdqfneallavassmqgwrnsedahmslfnfdn--tsfavydg 58
QY 61 HGGKLVAKFCAKHLHQEVLKSEAYAKGDLKASLEYSLRMD----- 101
DB 59 hggaeavaycadklphfklnketykngqfevalkeasflgfdktllqpsivslkilageh 118
QY 102 -----EMMKGASGWKELOSLETS----- 121

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PR	PR	01-JUL-1999;	PR	20-SEP-1999;	99US-0154779.

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Query Match 34.2%; Score 627; DB 21; Length 258;

Best Local Similarity 49.2%; Pred. No. 6.4e-50;

Matches 125; Conservative 43; Mismatches 76; Indels 10; Gaps 1;

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QY 340 QPKQSGVAASSTTD 353
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RESULT 14

AA080498

ID AA080498 standard; Protein; 210 AA.

XX AC

XX AC

XX AC

DT 17-OCT-2000 (first entry)

XX

DE Arabidopsis thaliana protein fragment SEQ ID NO: 6060.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence.
OS Arabidopsis thaliana.
XX
PN EF1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
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PR 09-MAR-1999; 99US-0123548.
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PR 27-AUG-1999; 99US-0151080.

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RESULT 15

AAG54775

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Search completed: June 19, 2002, 08:43:43
Job time: 238 sec

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PR	31-AUG-1999;	99US-0151438.
PR	01-SEP-1999;	99US-0151930.
PR	07-SEP-1999;	99US-0152363.
PR	10-SEP-1999;	99US-0153070.
PR	13-SEP-1999;	99US-0153758.
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PR	20-SEP-1999;	99US-0154779.
PR	22-SEP-1999;	99US-0155139.
PR	23-SEP-1999;	99US-0155486.
PR	24-SEP-1999;	99US-0155659.
PR	28-SEP-1999;	99US-0156458.
PR	29-SEP-1999;	99US-0156596.
PR	04-OCT-1999;	99US-0157117.
PR	05-OCT-1999;	99US-0157753.
PR	06-OCT-1999;	99US-0157865.
PR	07-OCT-1999;	99US-0158029.
PR	08-OCT-1999;	99US-0158232.
PR	12-OCT-1999;	99US-0158369.
PR	13-OCT-1999;	99US-0159293.
PR	13-OCT-1999;	99US-0159294.
PR	13-OCT-1999;	99US-0159295.
PR	14-OCT-1999;	99US-0159329.
PR	14-OCT-1999;	99US-0159330.
PR	14-OCT-1999;	99US-0159331.
PR	14-OCT-1999;	99US-0159637.
PR	14-OCT-1999;	99US-0159638.
PR	18-OCT-1999;	99US-0159584.
PR	21-OCT-1999;	99US-0160741.
PR	21-OCT-1999;	99US-0160767.
PR	21-OCT-1999;	99US-0160768.
PR	21-OCT-1999;	99US-0160770.
PR	21-OCT-1999;	99US-0160814.
PR	22-OCT-1999;	99US-0160880.
PR	22-OCT-1999;	99US-0160981.
PR	22-OCT-1999;	99US-0160989.
PR	25-OCT-1999;	99US-0161404.
PR	25-OCT-1999;	99US-0161405.
PR	26-OCT-1999;	99US-0161406.
PR	26-OCT-1999;	99US-0161359.
PR	26-OCT-1999;	99US-0161360.
PR	28-OCT-1999;	99US-0161361.
PR	28-OCT-1999;	99US-0161920.
PR	28-OCT-1999;	99US-0161992.
PR	28-OCT-1999;	99US-0161993.
PR	29-OCT-1999;	99US-0162142.
Query Match 32.0%; Score 588; DB 21; Length 293;		
Best Local Similarity 58.1%; Pred. No. 3.2e-46;		
Matches 111; Conservative 33; Mismatches 47; Indels 0; Gaps 0;		
QY	163	YSDFOQPIYGTAVVALIRGNKLFVANAGDSRCIMSRGAEVNLSDHKNLEHERKRE 222
DB	89	hsdfptsgtcacvalikdklfnagdsrvcvsksqaynlkdkpdlvekeril 148
QY	223	SAGGFVHGRRVNSLNLTRAIGDMFEFKGRDPLPDQKQVVTCCPDVVEVDLGGDEFIWA 282
DB	149	kaggfihagrringsnlktraigdmefkqnkflpsekqmvtdpdtidldcdddfllvva 208
QY	283	CDGIWDMSSQAVDFVKSRLPTTKTSLSSCEETILDYCLSPTRQOEGCDNMSIITVOPK 342
DB	209	cdgiwdmssqavdfvheqiksetkistvcekvdrclapdtatgedcdnmtilivqfk 268
QY	343	QSCVAASSTD 353
DB	269	knpseteped 279